

SEQUENCE LISTING

<110> Poulter, et al.

<120> UNUSUAL RETROTRANSPOSON FROM THE YEAST CANDIDA ALBICANS

<130> 674521-2001.1

<140> 09/430,590

<141> 1999-10-29

<150> 60/106,342

<151> 1998-10-30

<160> 156

<170> PatentIn version 3.0

<210> 1

<211> 388

<212> DNA

<213> Candida albicans

<300>

<308> AF043301

<309> 1998-07-21

<313> (1)..(388)

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tgctttttaag aaagagaggt tcaagtgggt taagtacgac ggtcacaaag attgcggctt	180
atgaggcccg aactgagttg aaatacaaaa tcaagatata attatatacc ttacttgtcc	240
atattgtttt ataatacatt cttcagatat ttaaatttct gtgtatcaac ctataaaaca	300
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<308> Y08494

<309> 1997-08-27

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tgaagaaaag aatataaaaa tataaaatat ataagaagac aaaggagaat ctctgaccct	180
tatatagacc gaaaactaga gtgacgatga accatcagac cagtcaataa ccaactaatt	240
taataatatc aataactcgt ctaacgaggt gtaaacaaaa taccgaaaat agaaatataa	300
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 <212> DNA
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<220>
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 <222> (398)..(1372)
 <223> ORF1 coding sequence for gag

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 <222> (1373)..(6103)
 <223> ORF2 - coding sequence for pol

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ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt	180
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt	240
acacgctcaa tctcaggtaa agaaagttha tattccatca gattagaagt cgatagtgat	300
aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt	360
gatagtttcg aagtttgaag gtacagaatt tcacaag atg agt tcc gca aag aat	415
Met Ser Ser Ala Lys Asn	
1 5	
gat gat aac gaa ggg aag gtc atg gaa agt gtt gat caa gct aat gct	463
Asp Asp Asn Glu Gly Lys Val Met Glu Ser Val Asp Gln Ala Asn Ala	
10 15 20	
att agt aag gtg gat gaa cat atc aag gct aga ttc aat atg ctt ttc	511
Ile Ser Lys Val Asp Glu His Ile Lys Ala Arg Phe Asn Met Leu Phe	
25 30 35	
ata aaa ttt aat gac tta cct aag ttg gcc gtc ggt aat cag aaa agc	559
Ile Lys Phe Asn Asp Leu Pro Lys Leu Ala Val Gly Asn Gln Lys Ser	

40	45	50	
gtg gat aaa tgg aat gaa gaa ttt aaa tat ttc cac gtt gct tac ccc Val Asp Lys Trp Asn Glu Glu Phe Lys Tyr Phe His Val Ala Tyr Pro 55 60 65 70			607
gat gtt ttg gaa ttt ttg ctt gac tat aat cct aaa gat aaa ttc aag Asp Val Leu Glu Phe Leu Leu Asp Tyr Asn Pro Lys Asp Lys Phe Lys 75 80 85			655
gtt aaa aag gta gaa ggt att tat ttt act ggt tgg tgt tta caa atg Val Lys Lys Val Glu Gly Ile Tyr Phe Thr Gly Trp Cys Leu Gln Met 90 95 100			703
tgt tta cag tcc att ttt gat agg ttc aga ttg atc atg att tct aag Cys Leu Gln Ser Ile Phe Asp Arg Phe Arg Leu Ile Met Ile Ser Lys 105 110 115			751
cta cca aag cac ttg caa aag gaa gca aac tta atc aaa gct gct tat Leu Pro Lys His Leu Gln Lys Glu Ala Asn Leu Ile Lys Ala Ala Tyr 120 125 130			799
gat gct gtt act aaa tct aaa gat tat acc att act agt aag atc ttg Asp Ala Val Thr Lys Ser Lys Asp Tyr Thr Ile Thr Ser Lys Ile Leu 135 140 145 150			847
ctg aag ttt gta aac gtt gaa cat gag tta gtg gtt tgc tat aac ctt Ser Lys Phe Val Asn Val Glu His Glu Leu Val Val Cys Tyr Asn Leu 155 160 165			895
cca tat ttg ctg cag gtg gaa gag aaa ctt gag gaa ata ctc tac aac Pro Tyr Leu Ser Gln Val Glu Glu Lys Leu Glu Glu Ile Leu Tyr Asn 170 175 180			943
act tca aac gtt gtc gat gag tat gtc cgt agt ctt cca aat ctc ata Thr Ser Asn Val Val Asp Glu Tyr Val Arg Ser Leu Pro Asn Leu Ile 185 190 195			991
ggt caa gtc ttg tac ttc aat cat gtg aag aaa tca gag gct tta agt Gly Gln Val Leu Tyr Phe Asn His Val Lys Lys Ser Glu Ala Leu Ser 200 205 210			1039
ttg ttt ttg aat att cat gcc tca tac tac tca aag tgg att caa gct Leu Phe Leu Asn Ile His Ala Ser Tyr Tyr Ser Lys Trp Ile Gln Ala 215 220 225 230			1087
gac aat gat aca tca gta ctc cca agt tgc tct acc ata gct gaa gaa Asp Asn Asp Thr Ser Val Leu Pro Ser Cys Ser Thr Ile Ala Glu Glu 235 240 245			1135
atg tgt gat cat cct gat tat gct aga ttg gtt gac att cca agc aac Met Cys Asp His Pro Asp Tyr Ala Arg Leu Val Asp Ile Pro Ser Asn 250 255 260			1183
aaa tat gaa ctt aat ctt att gtt agt tta cca gca cca gag aaa cca Lys Tyr Glu Leu Asn Leu Ile Val Ser Leu Pro Ala Pro Glu Lys Pro 265 270 275			1231

aaa gga aaa cca gag gag aac tca ctg gaa caa tct caa aag aag aac Lys Gly Lys Pro Glu Glu Asn Ser Ser Glu Gln Ser Gln Lys Lys Asn 280 285 290	1279
ctg aaa tca aga aag aga aat aag aaa cat cca aaa tca gat aac gat Ser Lys Ser Arg Lys Arg Asn Lys Lys His Pro Lys Ser Asp Asn Asp 295 300 305 310	1327
aaa ggt gaa aaa gaa aaa gaa aaa gaa aaa act tca ctg gaa tga aaa Lys Gly Glu Lys Glu Lys Glu Lys Glu Lys Thr Ser Ser Glu Lys 315 320 325	1375
aca ggt gct gct tct att aat tgt gta atg aat ata cat aat tgc agc Thr Gly Ala Ala Ser Ile Asn Cys Val Met Asn Ile His Asn Cys Ser 330 335 340	1423
aaa acc acg ttt cca gta gaa aat tct cat tct ctt aat gct tct ttg Lys Thr Thr Phe Pro Val Glu Asn Ser His Ser Leu Asn Ala Ser Leu 345 350 355	1471
aac gta atg aat ttt aaa ggt tta agg ttt aac aag tat cta gtg tat Asn Val Met Asn Phe Lys Gly Leu Arg Phe Asn Lys Tyr Leu Val Tyr 360 365 370	1519
gat act ggt gcc aca ata tct gtt gtg aac aat aaa gat ata ttg ctg Asp Thr Gly Ala Thr Ile Ser Val Val Asn Asn Lys Asp Ile Leu Ser 375 380 385	1567
aat gtt aag gac gca aca att gaa gtt tct gtt gct gat ggt gct aca Asn Val Lys Asp Ala Thr Ile Glu Val Ser Val Ala Asp Gly Ala Thr 390 395 400 405	1615
tta gaa gca gat tgt att ggt gat cta att atc aga gtc ggt att gtc Leu Glu Ala Asp Cys Ile Gly Asp Leu Ile Ile Arg Val Gly Ile Val 410 415 420	1663
tcg att acg tta gag aat aca ttg tat tta cca gaa agt tcc ttt aat Ser Ile Thr Leu Glu Asn Thr Leu Tyr Leu Pro Glu Ser Ser Phe Asn 425 430 435	1711
ctt gtg agt ttg aaa caa att gaa gaa cga gga ttt aat gtt ctt att Leu Val Ser Leu Lys Gln Ile Glu Glu Arg Gly Phe Asn Val Leu Ile 440 445 450	1759
act aaa gaa tca gtg att gta ttt aac caa aat gtg gct cct act att Thr Lys Glu Ser Val Ile Val Phe Asn Gln Asn Val Ala Pro Thr Ile 455 460 465	1807
att gct tca agg aag aat gct gct gat ctt tat atg ggt cct caa ttc Ile Ala Ser Arg Lys Asn Ala Ala Asp Leu Tyr Met Gly Pro Gln Phe 470 475 480 485	1855
agt gaa gaa tct tta gaa tgt gat ttt gat tat gat ggt ttg gca gat Ser Glu Glu Ser Leu Glu Cys Asp Phe Asp Tyr Asp Gly Leu Ala Asp 490 495 500	1903

atg ttg tcc aat gct aac caa gat gac aaa gat aaa tca agt atg aat Met Leu Ser Asn Ala Asn Gln Asp Asp Lys Asp Lys Ser Ser Met Asn 505 510 515	1951
gaa atg tca gaa tat caa gaa cat gat tat agt tct cga gca tta ata Glu Met Ser Glu Tyr Gln Glu His Asp Tyr Ser Ser Arg Ala Leu Ile 520 525 530	1999
aat tct ttg acg gag gtt gat gtt tta gat gtt gaa att tcc cca tat Asn Ser Leu Thr Glu Val Asp Val Leu Asp Val Glu Ile Ser Pro Tyr 535 540 545	2047
gga gtt gaa caa ttg cta cca act gga gat aag aac gat att tat aat Gly Val Glu Gln Leu Leu Pro Thr Gly Asp Lys Asn Asp Ile Tyr Asn 550 555 560 565	2095
ttc cat ttg atg tca aat cat atg tcc att gag aaa atc ttg ttg tta Phe His Leu Met Ser Asn His Met Ser Ile Glu Lys Ile Leu Leu Leu 570 575 580	2143
caa aaa tac cag ggt ctc gta ctt cac act tca aaa gag agt ctt caa Gln Lys Tyr Gln Gly Leu Val Leu His Thr Ser Lys Glu Ser Leu Gln 585 590 595	2191
aag att gct gat tgt aag gta tgt cta tta tcg aat gcc aaa cag aga Lys Ile Ala Asp Cys Lys Val Cys Leu Leu Ser Asn Ala Lys Gln Arg 600 605 610	2239
agt cac aat cat cat tca gaa aga aaa gcc tcg aga aga cat gag aga Ser His Asn His His Ser Glu Arg Lys Ala Ser Arg Arg His Glu Arg 615 620 625	2287
ctt cat tgt gat act ctc ggt cca ttt agg tcc gaa aat aac aag tgg Leu His Cys Asp Thr Leu Gly Pro Phe Arg Ser Glu Asn Asn Lys Trp 630 635 640 645	2335
tat tta acg tct gtt ata gat gaa cat acg ggt tac att gaa gga att Tyr Leu Thr Ser Val Ile Asp Glu His Thr Gly Tyr Ile Glu Gly Ile 650 655 660	2383
att act aaa gac aga aag gta aag gat ctc tta att caa cga tta aag Ile Thr Lys Asp Arg Lys Val Lys Asp Leu Leu Ile Gln Arg Leu Lys 665 670 675	2431
atc tgg aat aat cgg ttt aac gat aag gtg gca tac ttc aga agt gat Ile Trp Asn Asn Arg Phe Asn Asp Lys Val Ala Tyr Phe Arg Ser Asp 680 685 690	2479
aat gct cct gag ttc cca caa cct tct gat tta gct gag ttc ggt att Asn Ala Pro Glu Phe Pro Gln Pro Ser Asp Leu Ala Glu Phe Gly Ile 695 700 705	2527
tgg agg gag act ata gcg gca tat ctg cct gag ctt aat ggt ctc gcc Trp Arg Glu Thr Ile Ala Ala Tyr Ser Pro Glu Leu Asn Gly Leu Ala 710 715 720 725	2575
gag gtt gtt aat aaa ttg att tta caa cag att tac agg atc gtt gtg	2623

Glu Val Val Asn Lys Leu Ile Leu Gln Gln Ile Tyr Arg Ile Val Val	
730 735 740	
aca ctt ggt cca caa ata ctc aag ttg att tat tat gtg att caa tat	2671
Thr Leu Gly Pro Gln Ile Leu Lys Leu Ile Tyr Tyr Val Ile Gln Tyr	
745 750 755	
tct att aca atg atc aac cac act cca cgt cgt tca ctc aag gga caa	2719
Ser Ile Thr Met Ile Asn His Thr Pro Arg Arg Ser Leu Lys Gly Gln	
760 765 770	
acc cct tat ggt tgc tat tat caa tta agt gag gga aat ttc tac cgg	2767
Thr Pro Tyr Gly Cys Tyr Tyr Gln Leu Ser Glu Gly Asn Phe Tyr Arg	
775 780 785	
ttt cct ttt gcc atc gat tgt gtc gtt aca ttt agt aat gcc atc gaa	2815
Phe Pro Phe Ala Ile Asp Cys Val Val Thr Phe Ser Asn Ala Ile Glu	
790 795 800 805	
aag aac cgt tac gga gtt aca tca act aaa gga gct cct tca tcg atc	2863
Lys Asn Arg Tyr Gly Val Thr Ser Thr Lys Gly Ala Pro Ser Ser Ile	
810 815 820	
atg ggt gct gtg att ggc tac gct agc gat tgt ttt agt tat tac gtg	2911
Met Gly Ala Val Ile Gly Tyr Ala Ser Asp Cys Phe Ser Tyr Tyr Val	
825 830 835	
ttg cta aaa aat atg cgg tgt gat att atc ctt agc cct aat gtc cgt	2959
Leu Leu Lys Asn Met Arg Cys Asp Ile Ile Leu Ser Pro Asn Val Arg	
840 845 850	
ata ttg cga agc tat gag gtt att aac tcc tat ctc aaa aac tta tcc	3007
Ile Leu Arg Ser Tyr Glu Val Ile Asn Ser Tyr Leu Lys Asn Leu Ser	
855 860 865	
act aca cct atg tca cac att gtt cct atg gct gaa ggt atc cag gga	3055
Thr Thr Pro Met Ser His Ile Val Pro Met Ala Glu Gly Ile Gln Gly	
870 875 880 885	
agg caa ctg ggc gct cag tac gag gta cgc gga aca tat gtg gaa agt	3103
Arg Gln Ser Gly Ala Gln Tyr Glu Val Arg Gly Thr Tyr Val Glu Ser	
890 895 900	
gaa tat gac aat aca aat gac gtg atg cac atg ccc aaa gag tca tat	3151
Glu Tyr Asp Asn Thr Asn Asp Val Met His Met Pro Lys Glu Ser Tyr	
905 910 915	
tca gtt cag cca gca tcg ttt act tta act acg ggt aac agt tct aac	3199
Ser Val Gln Pro Ala Ser Phe Thr Leu Thr Thr Gly Asn Ser Ser Asn	
920 925 930	
gaa tat gtt ata aat gat gat cca gta cag att acc att gag aat ccc	3247
Glu Tyr Val Ile Asn Asp Asp Pro Val Gln Ile Thr Ile Glu Asn Pro	
935 940 945	
gat gat ttt tct aac cct ctt caa cta act gaa gaa tca cac gat atg	3295
Asp Asp Phe Ser Asn Pro Leu Gln Leu Thr Glu Glu Ser His Asp Met	

950	955	960	965	
gta tcc gaa gta aaa tcg gat gag aat cct aaa ccc agt ctc cac gag Val Ser Glu Val Lys Ser Asp Glu Asn Pro Lys Pro Ser Leu His Glu	970	975	980	3343
cta aca cct ggg gat aat ccg gtg tct aaa cct cct caa ctt ggt acc Leu Thr Pro Gly Asp Asn Pro Val Ser Lys Pro Pro Gln Leu Gly Thr	985	990	995	3391
gag act tca gta ata ggg aag tct aaa gag cct att aca aac cac Glu Thr Ser Val Ile Gly Lys Ser Lys Glu Pro Ile Thr Asn His	1000	1005	1010	3436
aca aag gac gcc cct tcc atc cag ggg agg gac cat aaa cgc ctg Thr Lys Asp Ala Pro Ser Ile Gln Gly Arg Asp His Lys Arg Ser	1015	1020	1025	3481
gaa tct act gct cag gtt gga cta tca cac caa ccc cag act ggt Glu Ser Thr Ala Gln Val Gly Leu Ser His Gln Pro Gln Thr Gly	1030	1035	1040	3526
act ccc gct tcg gag gag tca aaa ttg tca gga aca gat cat ttc Thr Pro Ala Ser Glu Glu Ser Lys Leu Ser Gly Thr Asp His Phe	1045	1050	1055	3571
ggt gtc gac gtt gtt aaa gaa aca gtc tca gaa gat tgg cat act Gly Val Asp Val Val Lys Glu Thr Val Ser Glu Asp Trp His Thr	1060	1065	1070	3616
tct gac tac cca gaa act agt gct gaa gat gaa cag caa aat ccc Ser Asp Tyr Pro Glu Thr Ser Ala Glu Asp Glu Gln Gln Asn Pro	1075	1080	1085	3661
tcg tta ctg gct aat aag aat cgg gta act gaa aaa ata gat gag Ser Leu Ser Ala Asn Lys Asn Arg Val Thr Glu Lys Ile Asp Glu	1090	1095	1100	3706
gga gaa aat att tca ttt ccg ggg ggt gat gat gat tct gtc gtg Gly Glu Asn Ile Ser Phe Pro Gly Gly Asp Asp Asp Ser Val Val	1105	1110	1115	3751
atc aac tca aat gtt gag caa tct aat gtt gaa aca gag gat gct Ile Asn Ser Asn Val Glu Gln Ser Asn Val Glu Thr Glu Asp Ala	1120	1125	1130	3796
ggt aac agt cca att caa gac gaa gtt tct caa gag gga aga ata Gly Asn Ser Pro Ile Gln Asp Glu Val Ser Gln Glu Gly Arg Ile	1135	1140	1145	3841
ctt aat gaa caa act gat ata gtt gat act gtt gct aaa gtt att Leu Asn Glu Gln Thr Asp Ile Val Asp Thr Val Ala Lys Val Ile	1150	1155	1160	3886
gag aat gaa aaa atc tct cct att aat tca tta gat gat cat act Glu Asn Glu Lys Ile Ser Pro Ile Asn Ser Leu Asp Asp His Thr	1165	1170	1175	3931

gaa ctt gct	aca gac tcg gga aat	gat agc aat tca aca	gaa tcc	3976
Glu Leu Ala	Thr Asp Ser Gly Asn	Asp Ser Asn Ser Thr	Glu Ser	
1180	1185	1190		
gac att caa	tcg aaa aat gaa ata	tca cca gtg att aat	gag aaa	4021
Asp Ile Gln	Ser Lys Asn Glu Ile	Ser Pro Val Ile Asn	Glu Lys	
1195	1200	1205		
aat act gaa	ata atc caa aaa cac	att gaa agt atc ctt	gct gat	4066
Asn Thr Glu	Ile Ile Gln Lys His	Ile Glu Ser Ile Leu	Ala Asp	
1210	1215	1220		
aag aga ttg	gat gaa ttt gaa acg	tat aat gtt gat gaa	att gag	4111
Lys Arg Leu	Asp Glu Phe Glu Thr	Tyr Asn Val Asp Glu	Ile Glu	
1225	1230	1235		
aat gtg att	aat gac gat gac att	gct gaa gct aat cca	cta cca	4156
Asn Val Ile	Asn Asp Asp Asp Ile	Ala Glu Ala Asn Pro	Leu Pro	
1240	1245	1250		
gat gaa aat	aat gat gtt cag atg	aat gag agt ttt gat	aat aat	4201
Asp Glu Asn	Asn Asp Val Gln Met	Asn Glu Ser Phe Asp	Asn Asn	
1255	1260	1265		
cat agc atg	tca cga gca aag aag	aaa tac aca ttt gag	aaa gaa	4246
His Ser Met	Ser Arg Ala Lys Lys	Lys Tyr Thr Phe Glu	Lys Glu	
1270	1275	1280		
gtt aac gaa	aaa att gct ggt act	aaa cat tca ctt gat	aca act	4291
Val Asn Glu	Lys Ile Ala Gly Thr	Lys His Ser Leu Asp	Thr Thr	
1285	1290	1295		
gat cca aga	gaa gca atc aga gtg	tta aat act ggt gaa	acc aag	4336
Asp Pro Arg	Glu Ala Ile Arg Val	Leu Asn Thr Gly Glu	Thr Lys	
1300	1305	1310		
aga atc gaa	ccc aag aaa aga gag	gtg cct atc act gtg	aaa tta	4381
Arg Ile Glu	Pro Lys Lys Arg Glu	Val Pro Ile Thr Val	Lys Leu	
1315	1320	1325		
aac aaa aga	tcg caa tac aag tca	cca tat gtt aca aga	agt ggt	4426
Asn Lys Arg	Ser Gln Tyr Lys Ser	Pro Tyr Val Thr Arg	Ser Gly	
1330	1335	1340		
aga acg gtt	ata aac ccc aag agg	tat tta cat gcg gtc	gtc aac	4471
Arg Thr Val	Ile Asn Pro Lys Arg	Tyr Leu His Ala Val	Val Asn	
1345	1350	1355		
aaa atc gac	tat aat gat ccg gga	tgg ata aag tca atg	aat gct	4516
Lys Ile Asp	Tyr Asn Asp Pro Gly	Trp Ile Lys Ser Met	Asn Ala	
1360	1365	1370		
gaa cta gag	aaa ttt aga tca aaa	gat gtt tac gaa gaa	gtt cca	4561
Glu Leu Glu	Lys Phe Arg Ser Lys	Asp Val Tyr Glu Glu	Val Pro	
1375	1380	1385		

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gag aaa att gat tct ctc aaa ggt gtt gtt cgg aaa tca cgt tgt Glu Lys Ile Asp Ser Leu Lys Gly Val Val Arg Lys Ser Arg Cys 1405 1410 1415	4651
gtt gtc cat ggc aac aga caa aag gaa aaa ttg gat tat gac cct Val Val His Gly Asn Arg Gln Lys Glu Lys Leu Asp Tyr Asp Pro 1420 1425 1430	4696
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ttg aca ata ata ggt tgt gaa tta gga atg aca att caa cat tta Leu Thr Ile Ile Gly Cys Glu Leu Gly Met Thr Ile Gln His Leu 1450 1455 1460	4786
gac gtc gag tcg gcg tat cta aat gcc tct att act cat tca aat Asp Val Glu Ser Ala Tyr Leu Asn Ala Ser Ile Thr His Ser Asn 1465 1470 1475	4831
cca att tat gtc ttt cct cct aaa tca gta cct ttg aag aaa aac Pro Ile Tyr Val Phe Pro Pro Lys Ser Val Pro Leu Lys Lys Asn 1480 1485 1490	4876
cat tgt tgg tta ttg aaa cgt tct gtc tat ggg tta aaa cag tcg His Cys Trp Leu Leu Lys Arg Ser Val Tyr Gly Leu Lys Gln Ser 1495 1500 1505	4921
ggt ttg gaa tgg tat cac act atc aaa aga gta ttg gaa gac att Gly Leu Glu Trp Tyr His Thr Ile Lys Arg Val Leu Glu Asp Ile 1510 1515 1520	4966
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gat caa ttg aga gat cat ttt gaa gtt aaa gtg ttt ggt gaa ata Asp Gln Leu Arg Asp His Phe Glu Val Lys Val Phe Gly Glu Ile 1570 1575 1580	5146
tca aat tat ctt ggt att gaa ttt cgt aaa acc gaa tct ggt tat Ser Asn Tyr Leu Gly Ile Glu Phe Arg Lys Thr Glu Ser Gly Tyr 1585 1590 1595	5191
att tta tct caa gaa aaa ttt ctc aag aaa tta ctt aag gat ttc	5236

Ile Leu Ser	Gln Glu Lys Phe Leu	Lys Lys Leu Leu Lys	Asp Phe	
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aaa cta gat	gac tca tat ggg aaa	aac ata ccc tgg att	ccg aat	5281
Lys Leu Asp	Asp Ser Tyr Gly Lys	Asn Ile Pro Trp Ile	Pro Asn	
1615	1620		1625	
gac aaa tat	gaa aag gtt gca ata	att cgt gaa aac gtt	aat cca	5326
Asp Lys Tyr	Glu Lys Val Ala Ile	Ile Arg Glu Asn Val	Asn Pro	
1630	1635		1640	
gag aat gat	ttt gaa aag gtt ccg	aat gag aca ttg ctt	gac cct	5371
Glu Asn Asp	Phe Glu Lys Val Pro	Asn Glu Thr Leu Leu	Asp Pro	
1645	1650		1655	
gat gct aaa	aaa cta tac caa agt	ggg gtt ggc ctg ctt	tta tgg	5416
Asp Ala Lys	Lys Leu Tyr Gln Ser	Gly Val Gly Ser Leu	Leu Trp	
1660	1665		1670	
gct gcc aca	aac aca cgt cca gat	ata tcg gtc gta gtg	aat tcg	5461
Ala Ala Thr	Asn Thr Arg Pro Asp	Ile Ser Val Val Val	Asn Ser	
1675	1680		1685	
ttg ggt tct	aaa tct gca aat cca	aat gtc cat gat tat	gag aaa	5506
Leu Gly Ser	Lys Ser Ala Asn Pro	Asn Val His Asp Tyr	Glu Lys	
1690	1695		1700	
ttg att tat	tgt ctt agg tat atc	aaa aat agc atg gga	tat cac	5551
Leu Ile Tyr	Cys Leu Arg Tyr Ile	Lys Asn Ser Met Gly	Tyr His	
1705	1710		1715	
att gag tac	aaa aga aac aga ttg	aat ata cca cca aaa	tca ttt	5596
Ile Glu Tyr	Lys Arg Asn Arg Leu	Asn Ile Pro Pro Lys	Ser Phe	
1720	1725		1730	
gtt atc gaa	tgt ttc agt gat gcg	tca ttt gca cca gga	ttg gat	5641
Val Ile Glu	Cys Phe Ser Asp Ala	Ser Phe Ala Pro Gly	Leu Asp	
1735	1740		1745	
aga aaa tct	att agt gga act ttg	att tat gtg aat gga	aat ttg	5686
Arg Lys Ser	Ile Ser Gly Thr Leu	Ile Tyr Val Asn Gly	Asn Leu	
1750	1755		1760	
gtg caa tgg	gcg acc aaa aaa caa	acg gtc ata gca caa	agc tca	5731
Val Gln Trp	Ala Thr Lys Lys Gln	Thr Val Ile Ala Gln	Ser Ser	
1765	1770		1775	
gca gct tgt	gaa atg ttg gct cta	aat tat aca atg ttg	aaa gct	5776
Ala Ala Cys	Glu Met Leu Ala Leu	Asn Tyr Thr Met Leu	Lys Ala	
1780	1785		1790	
atc gaa ata	aaa aac cat tta atg	gat ttg ggt ttt gaa	gta ggt	5821
Ile Glu Ile	Lys Asn His Leu Met	Asp Leu Gly Phe Glu	Val Gly	
1795	1800		1805	
aag ata cat	tgt cat caa gac aac	caa gct gtg att aaa	gtt ttg	5866
Lys Ile His	Cys His Gln Asp Asn	Gln Ala Val Ile Lys	Val Leu	

1810	1815	1820	
aga aat aac tat tgt cac cca cat	cga cca ata gat atc tgc tat	5911	
Arg Asn Asn Tyr Cys His Pro His	Arg Pro Ile Asp Ile Cys Tyr		
1825	1830	1835	
aag ttt cta cgc caa ttg atc aat	gat aaa gta ttt tca ata tcc	5956	
Lys Phe Leu Arg Gln Leu Ile Asn	Asp Lys Val Phe Ser Ile Ser		
1840	1845	1850	
tat gtg aag aca aat gat aat tac	gcc gat tgt atg act aag tgt	6001	
Tyr Val Lys Thr Asn Asp Asn Tyr	Ala Asp Cys Met Thr Lys Cys		
1855	1860	1865	
cta agt cgt gct aaa ttc aaa gca	ttc gtt gag ggt atg ata aaa	6046	
Leu Ser Arg Ala Lys Phe Lys Ala	Phe Val Glu Gly Met Ile Lys		
1870	1875	1880	
cgg tta gac cta gaa gat aat caa	aca ctg ata caa aat gca ata	6091	
Arg Leu Asp Leu Glu Asp Asn Gln	Thr Ser Ile Gln Asn Ala Ile		
1885	1890	1895	
acg gca gaa taa gtggatttat cattactatt atcgtaatgc tcaatcaggg		6143	
Thr Ala Glu			
1900			
gagtggttgtt ttgtgcacta ttttgtgtca gaaactgatc aatgaaaatg atggttatta			6203
tgagaatgga aaatttttcc atcacacatc aggtgatgac agaactaaac tatattgtgt			6263
agtataaata aggggtatgaa ataccaacat cccagaatat caacgagata gaagggagga			6323
gtttcaatat atatcttgtg aataataact tcgttctaata tcactataca caactagacg			6383
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<211> 324			
<212> PRT			
<213> Candida albicans			
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Met Ser Ser Ala Lys Asn Asp Asp Asn Glu Gly Lys Val Met Glu Ser			
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Val Asp Gln Ala Asn Ala Ile Ser Lys Val Asp Glu His Ile Lys Ala			
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Arg Phe Asn Met Leu Phe Ile Lys Phe Asn Asp Leu Pro Lys Leu Ala			
35	40	45	
Val Gly Asn Gln Lys Ser Val Asp Lys Trp Asn Glu Glu Phe Lys Tyr			

50

55

60

Phe His Val Ala Tyr Pro Asp Val Leu Glu Phe Leu Leu Asp Tyr Asn
 65 70 75 80

Pro Lys Asp Lys Phe Lys Val Lys Lys Val Glu Gly Ile Tyr Phe Thr
 85 90 95

Gly Trp Cys Leu Gln Met Cys Leu Gln Ser Ile Phe Asp Arg Phe Arg
 100 105 110

Leu Ile Met Ile Ser Lys Leu Pro Lys His Leu Gln Lys Glu Ala Asn
 115 120 125

Leu Ile Lys Ala Ala Tyr Asp Ala Val Thr Lys Ser Lys Asp Tyr Thr
 130 135 140

Ile Thr Ser Lys Ile Leu Ser Lys Phe Val Asn Val Glu His Glu Leu
 145 150 155 160

Val Val Cys Tyr Asn Leu Pro Tyr Leu Ser Gln Val Glu Glu Lys Leu
 165 170 175

Glu Glu Ile Leu Tyr Asn Thr Ser Asn Val Val Asp Glu Tyr Val Arg
 180 185 190

Ser Leu Pro Asn Leu Ile Gly Gln Val Leu Tyr Phe Asn His Val Lys
 195 200 205

Lys Ser Glu Ala Leu Ser Leu Phe Leu Asn Ile His Ala Ser Tyr Tyr
 210 215 220

Ser Lys Trp Ile Gln Ala Asp Asn Asp Thr Ser Val Leu Pro Ser Cys
 225 230 235 240

Ser Thr Ile Ala Glu Glu Met Cys Asp His Pro Asp Tyr Ala Arg Leu
 245 250 255

Val Asp Ile Pro Ser Asn Lys Tyr Glu Leu Asn Leu Ile Val Ser Leu
 260 265 270

Pro Ala Pro Glu Lys Pro Lys Gly Lys Pro Glu Glu Asn Ser Ser Glu
 275 280 285

Gln Ser Gln Lys Lys Asn Ser Lys Ser Arg Lys Arg Asn Lys Lys His
290 295 300

Pro Lys Ser Asp Asn Asp Lys Gly Glu Lys Glu Lys Glu Lys Glu Lys
305 310 315 320

Thr Ser Ser Glu

<210> 5
<211> 1576
<212> PRT
<213> Candida albicans

<400> 5

Lys Thr Gly Ala Ala Ser Ile Asn Cys Val Met Asn Ile His Asn Cys
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20 25 30

Leu Asn Val Met Asn Phe Lys Gly Leu Arg Phe Asn Lys Tyr Leu Val
35 40 45

Tyr Asp Thr Gly Ala Thr Ile Ser Val Val Asn Asn Lys Asp Ile Leu
50 55 60

Ser Asn Val Lys Asp Ala Thr Ile Glu Val Ser Val Ala Asp Gly Ala
65 70 75 80

Thr Leu Glu Ala Asp Cys Ile Gly Asp Leu Ile Ile Arg Val Gly Ile
85 90 95

Val Ser Ile Thr Leu Glu Asn Thr Leu Tyr Leu Pro Glu Ser Ser Phe
100 105 110

Asn Leu Val Ser Leu Lys Gln Ile Glu Glu Arg Gly Phe Asn Val Leu
115 120 125

Ile Thr Lys Glu Ser Val Ile Val Phe Asn Gln Asn Val Ala Pro Thr
130 135 140

Ile Ile Ala Ser Arg Lys Asn Ala Ala Asp Leu Tyr Met Gly Pro Gln
 145 150 155 160

Phe Ser Glu Glu Ser Leu Glu Cys Asp Phe Asp Tyr Asp Gly Leu Ala
 165 170 175

Asp Met Leu Ser Asn Ala Asn Gln Asp Asp Lys Asp Lys Ser Ser Met
 180 185 190

Asn Glu Met Ser Glu Tyr Gln Glu His Asp Tyr Ser Ser Arg Ala Leu
 195 200 205

Ile Asn Ser Leu Thr Glu Val Asp Val Leu Asp Val Glu Ile Ser Pro
 210 215 220

Tyr Gly Val Glu Gln Leu Leu Pro Thr Gly Asp Lys Asn Asp Ile Tyr
 225 230 235 240

Asn Phe His Leu Met Ser Asn His Met Ser Ile Glu Lys Ile Leu Leu
 245 250 255

Leu Gln Lys Tyr Gln Gly Leu Val Leu His Thr Ser Lys Glu Ser Leu
 260 265 270

Gln Lys Ile Ala Asp Cys Lys Val Cys Leu Leu Ser Asn Ala Lys Gln
 275 280 285

Arg Ser His Asn His His Ser Glu Arg Lys Ala Ser Arg Arg His Glu
 290 295 300

Arg Leu His Cys Asp Thr Leu Gly Pro Phe Arg Ser Glu Asn Asn Lys
 305 310 315 320

Trp Tyr Leu Thr Ser Val Ile Asp Glu His Thr Gly Tyr Ile Glu Gly
 325 330 335

Ile Ile Thr Lys Asp Arg Lys Val Lys Asp Leu Leu Ile Gln Arg Leu
 340 345 350

Lys Ile Trp Asn Asn Arg Phe Asn Asp Lys Val Ala Tyr Phe Arg Ser
 355 360 365

Asp Asn Ala Pro Glu Phe Pro Gln Pro Ser Asp Leu Ala Glu Phe Gly

370

375

380

Ile Trp Arg Glu Thr Ile Ala Ala Tyr Ser Pro Glu Leu Asn Gly Leu
 385 390 395 400

Ala Glu Val Val Asn Lys Leu Ile Leu Gln Gln Ile Tyr Arg Ile Val
 405 410 415

Val Thr Leu Gly Pro Gln Ile Leu Lys Leu Ile Tyr Tyr Val Ile Gln
 420 425 430

Tyr Ser Ile Thr Met Ile Asn His Thr Pro Arg Arg Ser Leu Lys Gly
 435 440 445

Gln Thr Pro Tyr Gly Cys Tyr Tyr Gln Leu Ser Glu Gly Asn Phe Tyr
 450 455 460

Arg Phe Pro Phe Ala Ile Asp Cys Val Val Thr Phe Ser Asn Ala Ile
 465 470 475 480

Glu Lys Asn Arg Tyr Gly Val Thr Ser Thr Lys Gly Ala Pro Ser Ser
 485 490 495

Ile Met Gly Ala Val Ile Gly Tyr Ala Ser Asp Cys Phe Ser Tyr Tyr
 500 505 510

Val Leu Leu Lys Asn Met Arg Cys Asp Ile Ile Leu Ser Pro Asn Val
 515 520 525

Arg Ile Leu Arg Ser Tyr Glu Val Ile Asn Ser Tyr Leu Lys Asn Leu
 530 535 540

Ser Thr Thr Pro Met Ser His Ile Val Pro Met Ala Glu Gly Ile Gln
 545 550 555 560

Gly Arg Gln Ser Gly Ala Gln Tyr Glu Val Arg Gly Thr Tyr Val Glu
 565 570 575

Ser Glu Tyr Asp Asn Thr Asn Asp Val Met His Met Pro Lys Glu Ser
 580 585 590

Tyr Ser Val Gln Pro Ala Ser Phe Thr Leu Thr Thr Gly Asn Ser Ser
 595 600 605

Asn Glu Tyr Val Ile Asn Asp Asp Pro Val Gln Ile Thr Ile Glu Asn
610 615 620

Pro Asp Asp Phe Ser Asn Pro Leu Gln Leu Thr Glu Glu Ser His Asp
625 630 635 640

Met Val Ser Glu Val Lys Ser Asp Glu Asn Pro Lys Pro Ser Leu His
645 650 655

Glu Leu Thr Pro Gly Asp Asn Pro Val Ser Lys Pro Pro Gln Leu Gly
660 665 670

Thr Glu Thr Ser Val Ile Gly Lys Ser Lys Glu Pro Ile Thr Asn His
675 680 685

Thr Lys Asp Ala Pro Ser Ile Gln Gly Arg Asp His Lys Arg Ser Glu
690 695 700

Ser Thr Ala Gln Val Gly Leu Ser His Gln Pro Gln Thr Gly Thr Pro
705 710 715 720

Ala Ser Glu Glu Ser Lys Leu Ser Gly Thr Asp His Phe Gly Val Asp
725 730 735

Val Val Lys Glu Thr Val Ser Glu Asp Trp His Thr Ser Asp Tyr Pro
740 745 750

Glu Thr Ser Ala Glu Asp Glu Gln Gln Asn Pro Ser Leu Ser Ala Asn
755 760 765

Lys Asn Arg Val Thr Glu Lys Ile Asp Glu Gly Glu Asn Ile Ser Phe
770 775 780

Pro Gly Gly Asp Asp Asp Ser Val Val Ile Asn Ser Asn Val Glu Gln
785 790 795 800

Ser Asn Val Glu Thr Glu Asp Ala Gly Asn Ser Pro Ile Gln Asp Glu
805 810 815

Val Ser Gln Glu Gly Arg Ile Leu Asn Glu Gln Thr Asp Ile Val Asp
820 825 830

Thr Val Ala Lys Val Ile Glu Asn Glu Lys Ile Ser Pro Ile Asn Ser
 835 840 845

Leu Asp Asp His Thr Glu Leu Ala Thr Asp Ser Gly Asn Asp Ser Asn
 850 855 860

Ser Thr Glu Ser Asp Ile Gln Ser Lys Asn Glu Ile Ser Pro Val Ile
 865 870 875 880

Asn Glu Lys Asn Thr Glu Ile Ile Gln Lys His Ile Glu Ser Ile Leu
 885 890 895

Ala Asp Lys Arg Leu Asp Glu Phe Glu Thr Tyr Asn Val Asp Glu Ile
 900 905 910

Glu Asn Val Ile Asn Asp Asp Asp Ile Ala Glu Ala Asn Pro Leu Pro
 915 920 925

Asp Glu Asn Asn Asp Val Gln Met Asn Glu Ser Phe Asp Asn Asn His
 930 935 940

Ser Met Ser Arg Ala Lys Lys Lys Tyr Thr Phe Glu Lys Glu Val Asn
 945 950 955 960

Glu Lys Ile Ala Gly Thr Lys His Ser Leu Asp Thr Thr Asp Pro Arg
 965 970 975

Glu Ala Ile Arg Val Leu Asn Thr Gly Glu Thr Lys Arg Ile Glu Pro
 980 985 990

Lys Lys Arg Glu Val Pro Ile Thr Val Lys Leu Asn Lys Arg Ser Gln
 995 1000 1005

Tyr Lys Ser Pro Tyr Val Thr Arg Ser Gly Arg Thr Val Ile Asn
 1010 1015 1020

Pro Lys Arg Tyr Leu His Ala Val Val Asn Lys Ile Asp Tyr Asn
 1025 1030 1035

Asp Pro Gly Trp Ile Lys Ser Met Asn Ala Glu Leu Glu Lys Phe
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Arg Ser Lys Asp Val Tyr Glu Glu Val Pro Ile Pro Thr Gly Val
 1055 1060 1065
 Lys Pro Ile Ser Met Gly Trp Val His Thr Glu Lys Ile Asp Ser
 1070 1075 1080
 Leu Lys Gly Val Val Arg Lys Ser Arg Cys Val Val His Gly Asn
 1085 1090 1095
 Arg Gln Lys Glu Lys Leu Asp Tyr Asp Pro Phe Ser Val Ser Ser
 1100 1105 1110
 Pro Val Ile Asp Leu Val Thr Ile Arg Leu Leu Thr Ile Ile Gly
 1115 1120 1125
 Cys Glu Leu Gly Met Thr Ile Gln His Leu Asp Val Glu Ser Ala
 1130 1135 1140
 Tyr Leu Asn Ala Ser Ile Thr His Ser Asn Pro Ile Tyr Val Phe
 1145 1150 1155
 Pro Pro Lys Ser Val Pro Leu Lys Lys Asn His Cys Trp Leu Leu
 1160 1165 1170
 Lys Arg Ser Val Tyr Gly Leu Lys Gln Ser Gly Leu Glu Trp Tyr
 1175 1180 1185
 His Thr Ile Lys Arg Val Leu Glu Asp Ile Gly Phe Thr Gln Val
 1190 1195 1200
 Leu His Asn Asp Gly Leu Phe His Ile Glu Tyr Glu Glu Gly Ser
 1205 1210 1215
 Val Ile Tyr Leu Gly Leu Tyr Val Asp Asp Ile Leu Met Val Gly
 1220 1225 1230
 Ser Ser Gln Lys Val Ile Asp Asn Phe Val Asp Gln Leu Arg Asp
 1235 1240 1245
 His Phe Glu Val Lys Val Phe Gly Glu Ile Ser Asn Tyr Leu Gly
 1250 1255 1260
 Ile Glu Phe Arg Lys Thr Glu Ser Gly Tyr Ile Leu Ser Gln Glu

1265	1270	1275
Lys Phe Leu Lys Lys Leu Leu 1280	Lys Asp Phe Lys Leu 1285	Asp Asp Ser 1290
Tyr Gly Lys Asn Ile Pro Trp 1295	Ile Pro Asn Asp Lys 1300	Tyr Glu Lys 1305
Val Ala Ile Ile Arg Glu Asn 1310	Val Asn Pro Glu Asn 1315	Asp Phe Glu 1320
Lys Val Pro Asn Glu Thr Leu 1325	Leu Asp Pro Asp Ala 1330	Lys Lys Leu 1335
Tyr Gln Ser Gly Val Gly Ser 1340	Leu Leu Trp Ala Ala 1345	Thr Asn Thr 1350
Arg Pro Asp Ile Ser Val Val 1355	Val Asn Ser Leu Gly 1360	Ser Lys Ser 1365
Ala Asn Pro Asn Val His Asp 1370	Tyr Glu Lys Leu Ile 1375	Tyr Cys Leu 1380
Arg Tyr Ile Lys Asn Ser Met 1385	Gly Tyr His Ile Glu 1390	Tyr Lys Arg 1395
Asn Arg Leu Asn Ile Pro Pro 1400	Lys Ser Phe Val Ile 1405	Glu Cys Phe 1410
Ser Asp Ala Ser Phe Ala Pro 1415	Gly Leu Asp Arg Lys 1420	Ser Ile Ser 1425
Gly Thr Leu Ile Tyr Val Asn 1430	Gly Asn Leu Val Gln 1435	Trp Ala Thr 1440
Lys Lys Gln Thr Val Ile Ala 1445	Gln Ser Ser Ala Ala 1450	Cys Glu Met 1455
Leu Ala Leu Asn Tyr Thr Met 1460	Leu Lys Ala Ile Glu 1465	Ile Lys Asn 1470
His Leu Met Asp Leu Gly Phe 1475	Glu Val Gly Lys Ile 1480	His Cys His 1485

Gln Asp Asn Gln Ala Val Ile Lys Val Leu Arg Asn Asn Tyr Cys
1490 1495 1500

His Pro His Arg Pro Ile Asp Ile Cys Tyr Lys Phe Leu Arg Gln
1505 1510 1515

Leu Ile Asn Asp Lys Val Phe Ser Ile Ser Tyr Val Lys Thr Asn
1520 1525 1530

Asp Asn Tyr Ala Asp Cys Met Thr Lys Cys Leu Ser Arg Ala Lys
1535 1540 1545

Phe Lys Ala Phe Val Glu Gly Met Ile Lys Arg Leu Asp Leu Glu
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Asp Asn Gln Thr Ser Ile Gln Asn Ala Ile Thr Ala Glu
1565 1570 1575

<210> 6

<211> 1309

<212> DNA

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<220>

<221> misc_feature

<222> (1)..(1309)

<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 6

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ttgaagcaaa agaaaagttt ggcatacagc tagatattta tatatgtata tgattagacc      180
aacataaaac tagacgtcca aatattttatt tattttattta ttgatataata ttctttattta      240
ttactgttat gatcttttga ttcacacaga gatttaatcc aaatcaatac cttttgtttt      300
gtagaaatct tttgtcttct caatttgtat tttcaattct ttgtatttat gttctttgtc      360
tttgaatgta acaattcccc aacctaacgt tgataaggca taagacccaa atgtgactaa      420
tccccaccat ggcaagtatg gcaatatttc atcgtgtatt ttagctggag ttggaatcac      480
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acctgtgata agagcaaaat aaatagctga taaggcaaaa attgttaatc ctgtttcagt	540
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acaatttctt cctttntctt ttctttgtat tantgggttag atttccattc catatacaca	1140
caagatgtca acgaaatcag caaattcaac tgctgtcaat tcatttaatg caaaccactc	1200
caactatgac gtttttagac cttcattcac cccagttttg gtcaatacat tcttagtaca	1260
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<210> 7
 <211> 1340
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature
 <222> (1)..(1340)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

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atgatggctc aatgattnat tttaggttta tatgtggatg atatcttaat ggacagaatc	180
tcagatggaa tcgttatcag atttgttgaa caagagagag tttatttcgc gtnaaaatca	240
atthaggtct catgacagaa tatgtgagat aaaatgtcca cgtaagcaaa actgggtgat	300
actntgaatt aagagatact cctaaataag caaccaagg atnttaaact acacaantcg	360
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gtcgcaaata ctgaanacaa tttcactgag gttcgaaatg naaaatnact taantcaatt	480
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gcgacgtttg tgcagggaa ataacacctt gatataagtc gtgcgtatta ggtcaacatt	840
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tatcaactgt actaataaag gagtgcattc tatgaccttt ggagaggaac tatgtataat	1260
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<210> 8
 <211> 556
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

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ggcgtaaact tcattcactc tgttttttgc ttattacaaa ttatcaccta tegtgtacta	180
ggactaatc tcacgaatat tccgtgtata caaacattat acgtgtctgt aactacgcga	240
aactacttcg tctcagtttt ttgttacaaa caactttccg tatagacctg agattttgtc	300
agcttgattg aatggaagag tttactaaag taccagaaag gtgttttata gataacatgt	360
agatatataa aaatgttata ttacaaatga cttccaaaag aaactgtacg aattttgctg	420

tttattaaaa accagttcct gaaaactagt atcttagctt cagtacattt agcccaccta 480
 aattggacct atgacaagtt ctactttccc gacaatgcta atatagagca gtttcttctt 540
 cttcttcttc ctgcgc 556

<210> 9
 <211> 2112
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 9

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 ccaattatta tcatcacctg cggagggttag tcaatttgag attgtgagag ggaaaaaaaa 180
 cgacctccat acactacctc aagtataagt ccagtcctaat tggtcgctat agagagattt 240
 cctagccgga atgcacgaca atcctgagac ggaagtcgat cgtcgatgcc catggtgcgt 300
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 tcaagtgggt taagtacgac ggtcaciaag attgcggctt atgaggcccg aactgagttg 420
 aaatacaaaa tcaagatata attatatacc ttacttgtct atattgtttt ataatacatt 480
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 gacgaacacc aatagtatga tgaagaactg accatggtgt aagagggttg atggagtttc 660
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 gtataacata agtttacatc aaatcagaat ttactaagaa aatcaatcca ttcaaaaggc 780
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 aagggttgaa tattgtttgg aaaattatat aattcatgtc aaactgggag gcttaaatga 900
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tttttatttc tgcattactg tttttagcaa atacacgtct aatttattgt atttgtaaa	1860
cattcttttc ctgaaatttt aagaaaatgt tttggtttgt tggaattcca tttaaacggt	1920
actttggggt gcagacagca atccatttgg agagtggcaa gtctacacga atttagctaa	1980
ggttcactat atcgtgtaac aagaaatttc tataccaaat aaacagcact tgattgaact	2040
acaatatgta aaaacttgct tttattacca gtcttcatac ataccccggt cttctctttt	2100
caatattctg ta	2112

<210> 10
 <211> 3742
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 10

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atcagcatac atggccccga aaactacttt accgtgtcgc tttaaccccc ccttcctaa	180
aacgagacaa ttagacatac attccacaat tatcataatc cccttttttt tccttacaaa	240
acactttatt tttgtcgttt tcgttatttg cttcgacgac attgtaaact ctttggaatt	300
gcagtagtag tgctcctggt gtaagggtggg tttggttgta gagtaaaaga aacgacaatt	360
gattacacct cgatatgcat acgcatggca aagagaatac cgagttaata gtgagtctat	420
tagtggtgca ggaaaagtta tacgaacaac attttgttta gtgtggatat tccagatcaa	480

caacaatatg actaaatca tagctctaatt tttcagttta cctttgttta ttacgataact	540
gccacagtcg tgcgtgtagca gggtcagttt tagaaaaact attctagaaa tgatgagtag	600
aatgtacta ttatgagcaa tatttcaaaa agtgaaatta taattgctgc tgacaacacc	660
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tggtcgttgt cgtcattgtc gattagtttc agtttctaga ggtgaaattt tctatggcac	780
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ctgcctatac ctgatataca catggcacat ggcgtatccc acaaaaaacc gtcaagacaa	2340
caccaatatg acaatgccaa ttatacaatt gcatatacca cgtgacttca ttttatggtc	2400
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ttcctagccg gaatgcacga caatcctgag acggaagtcg atcgacgatg cccatggtgc	2520
gtggtgaaaa attttcttag aaaatttggt ctttcttca actgctttga agaaagggag	2580
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tattgtatat atattattaa tgttatatta cactattgtt tgtttgttg ttataattat	3660
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agctatcaat ggctccacgt tt	3742

<210> 11
 <211> 1438
 <212> DNA

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<220>

<221> misc_feature

<222> (1)..(1438)

<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

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atgcacgaca atcctgagac ggaagtcgat cgtcgatgcc catggtgcgt ggtgaaaaat	180
tntcttagaa aatttgttct ttccttcaac tgcttttaag agaagggagg ttcaagtgg	240
ttaagtacga cggtcacaaa gattgctggct tatgaggccc gaactgagtt gaaatacaaa	300
atcaagatat aattatatac cttacttgtc tatattgttt tataatacat tcttcagata	360
tttaaatttc tgtgtatcat cctataaaac agagatacat tcagtacatt tagtatactg	420
agtgaactgg tacctgtgac attcaagata actgtttcgc gcacgctggc agacgaacag	480
caattctgta attgtcgtag agtagcaaca aatcttcccg atgattggta cttgtgttag	540
tctacacgac atgtgttttg gtacacttga actgtatgtc caagaatgga aacatatgcg	600
ggaaggacgc gaaagatgag tttggtatag aaggataag aactgtaaaa tatattatgt	660
agttatatat tttaattatg ggaaattgag tgtttattct gttcaacaag tttcaaccgt	720
agagattaca tttaaagtct gtggtcgaaa tccacaagat acagcaaatt catgaattca	780
cctattttaa tcaagtttac caagcaccat tgcctagaac ttgccatata atcaattaag	840
tcagacatta ctaatttgag caaagctttt agcttaatgg gccaaactaat ttaagtcgaa	900
ttggtaatgc aatctgttct tcatttgagt cgcttgctac ggctccatga cacatccatt	960
tgattgtttt aattcgagca attatccacc ataactctca gtaatatcat taacagtttt	1020
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tatatacgac cagtaaagag tgtgatgagg tgtttactgt aggttaaatt gcaattgact	1140
tgagttgata gcggttatta caaaagtata gattcaacaa attaagacaa gtaccaaacg	1200
ataggccgaa tgtgacttat accgttgaag ttcaagcgtt tttaacaaat agaaatgtga	1260
gattaatgag ttcgacaaat gttttactag atactattaa ttctgatgta ctatataagt	1320
ttaaccagct ataaccggca gagcagactt cctgaaactc aaattgggtg tgtttgact	1380

tgagttacac caciaaagttt gacaatcgtg aggacatagc aacctatcaa gccactca 1438

<210> 12

<211> 1304

<212> DNA

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 12

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ggagaaaaat cttttaacag acattgtata aacgttgaag attaaagaaa aaaaaaacag 180
aaagattacg aataatttgt ttttaattgg tgggtatgag gtgttgcgca gtgcactcaa 240
caattctctt ttggtgcaca aagttggttt tatggtcaac aattacggag tactgtctgt 300
agtgatgttg aatctaagac ggaaatgcct cctttacatt tgtttctatt ctcttaaaat 360
acatattcaa ttgtgtgttt taattgaaaa tttgttcac ttcatctgat gattgtgtaa 420
tctttgcggg gggggggcgt gtcatgaacc aatctctttg agtcatagga cgagtcattc 480
tattgtgact catggctcat cttactctct tactaatctc ttacttcac ttgtttactat 540
aaatatgtct actactctc tattttatta cctcgtttac tatttttatt caatatatga 600
tcttatcttt aaatttcttt tgacaaatac aatcaactta caaaacaaaa gaaaaaagac 660
taataaaata gaattaatga aaaaaaaaaa agactaataa aagaaaaaga aagaagacta 720
acaaaagaaa aaacaaaccg gagaaccctt cgctgtagag gaatttccta gccggattgc 780
acgacaatcc tgagacggaa ttcatcgtt gatgaccgtg gtgcgagggtg aaaagttttc 840
gtagaaattt tgttctctct ttcaaactgc ttttaagaaa atgagggttca agtgggttaa 900
gtacgacggt caciaaagatt gcgacttatg aggaccgaac taagttgaaa taaaaaatca 960
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gtaaaaaaaa aaatattgaa gaacctcatc accaagatgt ttgaaaaaaaa aaaaaatcaa 1200
atacttaatc gcaagctttt caattttattg attgtttgaa ttaattgaat ataaacaaaa 1260
aaaaaaagaa ttcaaattca ttgacatgt cagtgggaagt taga 1304

<210> 13
<211> 3604
<212> DNA
<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<220>

<221> misc_feature

<222> (1)..(3604)

<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 13

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tcttgctgct gaaagaattg gaaaagctct ttccagtnac aatctaactg agagaacttg      180
aaagggatca gcatttttgt tatgtcaaca tttaatgacc aatgaccacc agcacgatga      240
tattattctt aaattttctg ttagcgggtgt ctcaccatgg tacttacatc tgcaaattta      300
catgctgtca tataaacttg gattctcaaa ttgttttta gagatttatg ctcaacatta      360
tgaattgtat aaagcagatc ccatttaca attgccagat agtatgacat tgttgaatga      420
aataagatca aatagagatt atcctaaagt ggtaaagtct gcaaaaaata cagtacaagt      480
caataatggt tcatccaaga acaataaaaa gaaggatgaa tgacaacaat tagccaataa      540
aattgaggaa gtaggacgtt atagcgaaat aaacgcaaca tctacatata atgaaattgg      600
cgataccaac aaaaaccaa ggacaattaa tattgaattt gaaaaatcat acaaaattaa      660
gtgaacaaaa gaagaaaaca aacctattgg tatatgatct gggagccaca gtatccgtgg      720
tgaatgataa gactttactt aacgacatta aagaatcaaa tatcgaaatt gcaactgctg      780
aaggggagac atctacggct tatgcttttag gtactctaac catatctgtg aatggattga      840
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aacaatttga agatttatgc tacgcaattt tgatttccga aaatttaatg tttctagtgc      960
acagtgacca cgaacctacg gtcattgcga aatattcacc taaagatgac ttatactcag     1020
gccaagatc gggaaacttt cttaagaaga atcataatga acaaaaccaa attttgcttg     1080
acactgctaa aaaactatta ggatcagaga acatatttct ggagaaatca ctgaaaaatc     1140
caatgattga tcaaggaaaa ttagatccgt tgaaaatgaa caataaagta gaaagagtta     1200
actatgtcag catacacaac atcaaacaag aagtggcaga caaatatatg ataaaagatc     1260
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agatatgtgt tgcagcccat gcaaaattag ctagccataa tcacactcaa caacgggaat	1440
tggagcgacc attacaacgc ctccatttgg ataccgccgg accattttacc tcaaataaaa	1500
ctaagagcta tcttacaacc gtgattgatc aattttccag atatactgaa gttattgtat	1560
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ttagttgtca agtattaata cttttcccat ttatagtga gtatgcgggt catatccgga	1860
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 ggcc 3604

<210> 14
 <211> 995
 <212> PRT
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
 <221> UNSURE
 <222> (1)..(995)
 <223> 'XAA' can be any amino acid

<400> 14

Met Lys Leu Ala Ile Pro Thr Lys Thr Lys Gly Gln Leu Ile Leu Asn
 1 5 10 15
 Leu Lys Asn His Thr Lys Leu Ser Glu Gln Lys Lys Lys Thr Asn Leu
 20 25 30
 Leu Val Tyr Asp Ser Gly Ala Thr Val Ser Val Val Asn Asp Lys Thr
 35 40 45
 Leu Leu Asn Asp Ile Lys Glu Ser Asn Ile Glu Ile Ala Thr Ala Glu
 50 55 60
 Gly Glu Thr Ser Thr Ala Tyr Ala Leu Gly Thr Leu Thr Ile Ser Val
 65 70 75 80
 Asn Gly Leu Asn Ala Lys Leu Asp Gly Val Leu Tyr Leu Pro Ser Ile

85	90	95
Gln Leu Asn Leu Ile Ser Ile Lys Gln Phe Glu Asp Leu Cys Tyr Ala 100	105	110
Ile Leu Ile Ser Glu Asn Leu Met Phe Leu Val His Ser Asp His Glu 115	120	125
Pro Thr Val Ile Ala Lys Tyr Ser Pro Lys Asp Asp Leu Tyr Ser Gly 130	135	140
Pro Arg Ser Gly Asn Phe Leu Lys Lys Asn His Asn Glu Gln Asn Gln 145	150	155 160
Ile Leu Leu Asp Thr Ala Lys Lys Leu Leu Gly Ser Glu Asn Ile Phe 165	170	175
Ser Glu Lys Ser Ser Lys Asn Pro Met Ile Asp Gln Gly Lys Leu Asp 180	185	190
Pro Leu Lys Met Asn Asn Lys Val Glu Arg Val Asn Tyr Val Ser Ile 195	200	205
His Asn Ile Lys Gln Glu Val Ala Asp Lys Tyr Met Ile Lys Asp Leu 210	215	220
Tyr Tyr Tyr His Leu Leu Ile Asn His Leu Ser His Glu Lys Leu Gln 225	230	235 240
Leu Leu Val Lys Arg Gly Val Ile Lys Pro Val Lys Ser Thr Ser Ala 245	250	255
Glu Ser Ala Ile Leu Asn Cys Gln Ile Cys Val Ala Ala His Ala Lys 260	265	270
Leu Ala Ser His Asn His Thr Gln Gln Arg Glu Leu Glu Arg Pro Leu 275	280	285
Gln Arg Leu His Leu Asp Thr Ala Gly Pro Phe Thr Ser Asn Lys Thr 290	295	300
Lys Ser Tyr Leu Thr Thr Val Ile Asp Gln Phe Ser Arg Tyr Thr Glu 305	310	315 320
Val Ile Val Ser Asp Thr Lys Ala Val Lys Gln Ser Ile Leu His Arg 325	330	335
Leu Arg Val Trp Asn Asn Arg Phe Gln Phe Lys Ile Ala Glu Ile Arg 340	345	350
Tyr Asp Asn Ala Leu Glu Tyr Pro Ser Ala Glu Glu Leu Glu Glu Leu 355	360	365
Gly Ile Tyr Lys His Leu Leu Pro Asn Tyr Ser Pro Met Leu Asn Gly 370	375	380
Thr Ala Glu Ala Thr Asn Arg Pro Ile Val Gln Gly Ile Tyr Lys Val		

385	390	395	400
Val Leu Asn Phe Ser Cys Gln Val Leu Ile Leu Phe Pro Phe Ile Val	405	410	415
Glu Tyr Ala Val His Ile Arg Asn His Thr Pro Ile Lys Glu Phe Asp	420	425	430
Gly Ala Thr Pro Tyr Glu Arg Tyr Tyr Gly Leu Ser Lys Tyr Val Ile	435	440	445
Pro Phe Phe Gln Phe Gly Thr Asp Val Leu Ile Lys Cys Ala Ser Val	450	455	460
Gln Glu Ala Ile Ser Leu Lys Leu Pro Ser Ser Arg Asp Lys Ala Phe	465	470	475
Pro Thr Val Met Phe Gly Ala Phe Leu Gly Tyr Gly Ser Asp Ser Phe	485	490	495
Thr Phe Arg Val Leu Val Ser Thr Lys Gly Tyr Pro Val Ile Thr Thr	500	505	510
Ser Asn Ile Arg Pro Ile Ala Thr Met Gln Val Leu Asn Asp Tyr Leu	515	520	525
Ala Tyr Ile Ser Glu Asn Ser Ser Ile Ser Tyr Asp Asp Thr Phe Leu	530	535	540
Ser Pro Leu Asn His Pro Met Ile Arg Thr Asn Gln His Asp Arg Arg	545	550	555
Gly Asp Asn Ile Asn Val Glu Tyr Glu Asn Arg Pro Asn Val Pro Phe	565	570	575
Glu Tyr His Ala Glu Pro Pro Arg Thr Asn Ser Ser Thr Gly Ile Ile	580	585	590
Asp Arg Pro Asp Ile Arg Pro Arg Ala Asp Pro Thr Trp Gln Arg Met	595	600	605
Pro Asp Ala Asn Ile His Gln Glu Thr Thr Thr Val Gln Thr Pro Asp	610	615	620
His Gly Glu Leu Asp Thr Met Ile Asn Asn Glu His Gln Leu Pro Arg	625	630	635
Ser Gly Glu Gly Asn Tyr Pro Gly Gln Gln Val Arg Thr Asp Ile Ile	645	650	655
Gly Gln Phe Arg Asp Arg Gly Pro Thr Thr Leu Asn Thr Pro Ile Asp	660	665	670
Leu Gly Val Pro Asp Glu Thr Asp Asp Ile Ser Met Thr Ser Glu Asn	675	680	685
Pro Ile Asp Ser Pro Asn Ser Glu Met Ile Ile Ser Pro Ser Leu Pro			

690	695	700
Thr Asn Glu Leu Glu His Gln Ile Asp Ile Ser Ser Gly Glu Met Ser 705 710 715 720		
Leu Leu Gln Thr Asn Met Glu Ala Asp Asn Glu Leu Lys Thr Asn Glu 725 730 735		
Met Val Leu Tyr Lys Ser Lys Asn Asp Gly Ile Ile Ile Gln Gln Gln 740 745 750		
Gln Phe Thr Glu Asn Leu Ser Asp Glu Asn Glu Glu Asp Ser Ser Thr 755 760 765		
Asp Glu Glu Thr Leu Glu Asp Lys Lys Gln Gln Arg Leu Glu Tyr Asn 770 775 780		
Ile Ser Pro Asn Asp Glu Trp Ile Asn Asn Asp Val Gln Asn Glu Asp 785 790 795 800		
Asp Thr Gln Val Pro His Val Lys Glu Pro Ile Asn Tyr Glu Thr Gln 805 810 815		
Ser Arg Asn Gly Thr Asn Met Pro Arg Ile Glu Met Gly Ile Ile Glu 820 825 830		
Asn Leu Ser Asp Asp Gly Lys Asn Thr Pro Arg Glu Leu Arg Met Val 835 840 845		
Thr Tyr Asp Asn Asn Lys Lys Ile Gln Lys Tyr Gln Asn Ser Asn Ile 850 855 860		
Glu Ile Ser Glu Pro Arg Asn Glu Asn Lys Asn His Thr Phe Ile Glu 865 870 875 880		
Ser Asn Leu Glu Leu Leu Asp Asn Gln Glu Met Phe Gln Glu Asp Pro 885 890 895		
Gln Val Glu Asp Ile Arg Leu Thr Thr Pro Lys Lys Asp Lys Ser Leu 900 905 910		
Ser Pro Asp Phe Asn Gln Thr His Asn Glu Ile Gln Leu Phe Met Ala 915 920 925		
Asp Ile Asn Glu Asp Met Leu Glu Glu Tyr Asp Glu Asn Ile Asn Met 930 935 940		
Asn Glu Val Leu Ala Asp Ser Thr Glu Thr Leu Asp Lys Glu Leu Asp 945 950 955 960		
Leu Asp Glu Glu Ser Gly Arg Ile Glu Tyr Ile Ala Asp Arg Val Arg 965 970 975		
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Lys Asn Gly		

995

<210> 15
<211> 1249
<212> DNA
<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 15

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atagacaaaa cagcaaataa ggttgcaaaa gtagcccaaa caaactagat ttcggttacg      120
aattttccat ctttcaaaac aatgaatttg tttagagctc tgtgccattt attgcaacta      180
aaatgaatat gcaattaaac aatcagagat gtattggatt atccccgtgg tatacttttg      240
agttcaccat ttgttttttt tttgggggta aattagtgtc cctactaaaa atcgcattha      300
tcttacactc accattttga taagttatct ctgggtcaatc gcaaatacta tgcttctaata      360
taagagttct atgtaaatcc catttaattt tgatcaatct attggtttga agtaagagtt      420
gattttctgt aaagatttat ttggccagtg tagttcgggtg tcaaaaatat attatgatgt      480
acactaaaaa acactaaatt tcaagtcaat ggggaacaca aaactgaatt aattactata      540
tgttggtttg tgcactatth tgtgtcagaa actgatcaat gaaaatgatg gttattatga      600
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat atttgttagt      660
ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gagaggagtt      720
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt      780
acacgctcaa tctcaggtaa agaaagttta tattccatca ctatataaca acaatcaggc      840
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tacgcacgtg gcacccctta tctattttatt caatttacct ctaatttatg aattagctta      960
ataagagcag tcaaattaac acggctcaat taatagtact taataatatg aagccgatca     1020
attaaccgat cctttgaata atttgaaaat aaaataaagt aatataaata ggtatgcatt     1080
ttccctacat ttatttcctc tttctatttt aatttgtttc ctaaacagca acaacaacaa     1140
ttgaaattca aaaatgggtt ctgtttctaa attattgaac aatggattgt tattagctgg     1200
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<210> 16
<211> 5611
<212> DNA

<213> Unknown

<220>

<223> sequence of retrosequence of retrotransposon from unknown organisms

<220>

<221> misc_feature

<222> (1)..(5611)

<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 16

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atagacaaaa cagcaaataa ggttgcaaaa gtagcccaaa caaactagat ttcggttacg	120
aattttccat ctttcaaaac aatgaatttg ttagagctc tgtgccattt attgcaacta	180
aaatgaatat gcaattaaac aatcagagat gtattggatt atccccgtgg tatacttttg	240
agttcaccat ttgttttttt tttggggtta aattagtgtc cctactaaaa atcgcattha	300
tcttactctc accattttga taagttatct ctggtcaatc gcaaatacta tgcttctaata	360
taagagttct atgtaaatcc catttaattt tgatcaatct attggtttga agtaagagtt	420
gattttctgt aaagatttat ttggccagtg tagttcgggtg tcaaaaatat attatgatgt	480
acactaaaaa acactaaatt tcaagtcaat ggggaacaca aaactgaatt aattactata	540
tgttggtttg tgcactatth tgtgtcagaa actgatcaat gaaaatgatg gttattatga	600
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt	660
ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gagaggagtt	720
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacaca ctagacgtgt	780
acacgtcaa tctcaggtaa agaaagttta tattccatca ctatataaca acaatcaggc	840
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ataagagcag tcaaattaac acggtcfaat taatagtact taataatatg aagccgatca	1020
attaaccgat cctttgaata atttgaaaat aaaataaagt aatataaata ggtatgcatt	1080
ttccctacat ttatttctc tttctatttt aatttgtttc ctaaacagca acaacaacaa	1140
ttgaaattca aaaatgggtt ctgtttctaa attattgaac aatggattgt tattagctgg	1200
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cgtcaattct cttggcggta gtgcccctta tattcaaaga aacggatatg ggatttctac	1320

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caaaggtact tttaaagggtg atttggcttt cttaaagtat tatacttatt ttgttactga	1500
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aaccaatgcc ttgctgcacg gtgctgcgtt tagagccaaa tatggatcct tatacaagga	1620
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tgctgaaaga ttagttaaac caaaccagg tttgaatttg actacaagtg atgtcaacaa	1920
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ctatccaaaa tacaaaattt tactgcaaac tcctgaagtc gatcgtgaat actacaaaaa	2940
catcaccagt cctgaattca ttagacaatg gcagccagaa gtcctcaatc actaccgaaa	3000
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tttgagaatc caaaagtttt tccatccatc catcttaccg aatgaacttc atggcgatgt	3120
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tcttcaaaat tatgttagag atagctccaa cagtaaatac acttattatc gttgtgagta	3240
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acaaaataga acaataatg agcaaatac cccaaatgaa attatcacag aagttgacgg	4200
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caaactcaaa gcagaagcag tttcagatga ggacatgagg caaatgattg ttgaccttc	4740

aggttatatt gcagttaaat cgttcaatgg atcaaattat tacaagatta gttttggtga	4800
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aatgatcca gatggtgacg aaccagattt tagtattgaa aacacagaac caactgaagt	5160
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tgggttctcc atagatgacg acaatattgg aaacgacttc gaactcgctg actcttctca	5280
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cgaaagcata gaaggggttt atgctaagaa agctgctaga aatattaagc aacgggaaga	5460
gaattatagt agtttagata cagagggttaa aagaattcaa gatgaggaga aatctcaaag	5520
ggagaagggt aaaaagctaa gggcattaat taaaaaagaa gagatggaac ataaaaagaa	5580
aatggcggca gtgaatagga ttcaaaagaa a	5611

<210> 17
 <211> 1308
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature
 <222> (1)..(1308)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 17	
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ttgttataca tcattttttt tttttgcttt gtctcacga atattatttg attcctaaaa	120
aattgtaata ccctgtgttg gtttgtgcac tattttgtgt cagaaactga tctatgaaaa	180
tgatggttat tatgagaatg gaaaattttt ccatcacaca tcaggatgatg acagaactaa	240
attatattgt gtagtataat aaagggtatg aaataccaac atcccaggat atcaattata	300
tagaagggaa ggagtttcaa tatatatctt gtgaataata acttcgttct aattcactat	360

tcacaactag gcggtgtacac gctgaatctc aggtaaagaa agtttatatt ccatcactct	420
gaagtcatac attaataatta aataaacaat ctaacactag catgcattca taacctatag	480
atcattctaa acaagctggt aacacaaatc caatcaattg aatttatcat ataatgaagt	540
aacttttttc aaggcaacat ctattctttt attaattctcg acgtctgttt gattaagttg	600
ctctaacatt ttatttagat ccttctctat attttctgca atatcaaaca ccgattgctt	660
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tgttactgac agattggcac tgacattacc tgaattgttc atgtttgctg ttgaaagagc	780
aggaactgta cttggataag cagccgattc aaaagaagat gtggacatga gtgtcaagaa	840
aatgtgtaga atcagtacaa gactggaaaa cagaaggaac aaagtgaact ggatattgta	900
gttttgttga tagtactcgc gagctttaat tttttttgt aactggcggga atcagatctt	960
atgcaatact caaatccaaa gaaacagtca atccagatga aaggcatgta atcgctagtt	1020
ttcataaaca gaatcatggt actagtcata ttttctataa aaattcaata cttcattctt	1080
tttgttcaat actaactata aatgcttaca aatagattca aatttcaacc agatccacca	1140
cttcattagg ctcaaccaat ttttcataaa tagaaacgtc ttcttcagcc aagcttaatt	1200
gatgggaaac cctagcttgc attgaaggaa aaatacataa tccaaataac aaactgtctt	1260
tcnnaatatt ctcaaaattc gacttcaccg ttttccaacc aagcaggt	1308

<210> 18
 <211> 1672
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature
 <222> (1)..(1672)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 18	
cctatcaggt acttccccac ttggattggc ttctgcctct cttcttctcc caaccatcat	60
cccaatatca ttccacccat cgtcttcacg gttgtcgtct tttgttggtg tctcttcttg	120
tttttctagt ttaccactat aaaaatcaat caattcagtt tgttttatgg catcagattt	180
ataaattttt ttaattttat caacataatt atcaacaatc caatcaagat gtaatttatt	240

caatTTTTct tgtaaagaat caccaccacc atttcctatt ccttccattc ttgataatat	300
attccaatta gtttcatgac ataatttcgt taattcatct aaatcattca attggtgttt	360
atcattaata atttgattta tattgatgga aattttatca attaaatttt tagaaatttt	420
agaatttaaa taatttttga ttataggata ttgtaattca ttataaaatc taattaaatt	480
agtaattgat ttaataaaat tgttgcctc gttgtctgat acaatttcta atttaatagt	540
atcttccaat tcatcaacaa tcaaactaag ttgttttgaa ggggtggggg tggagtcccc	600
caatattgaa tccactaatt tatcccaatt ttccttatat ttatcgtatg cattcatatt	660
attatgtcca tttttcaata aaaaccgatt gaaatcttgt aaaattgcta tattagtaat	720
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tgttttcggt ttcccaaat acgtttcaat ttcttttaat ttagaattga tctcttgtaa	960
ttcattcaat tgttgtaa atgtcagtaac gatttcaaat ttattattca attcagtaat	1020
tgttaaatca gttaaattgt tactttcagt ggtatttgaa tcttgaggaa tttcttcaaa	1080
ttgttttcgg aaatcattat cattttcaag ggtgttttg tttattttgg ataatgtttt	1140
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cgatggcatt attggtgttg tataaaaatg gaattttgta aagttgaatg tgttggcaac	1260
acttgtgttt gtatgggcgt atattttttg aggagatcaa agcaaaaaat attttgagac	1320
ttatacacgc aacatacaga acagttgttg gtttgtgcac tatttttgtgt cagaaactga	1380
tcaatgaaaa tgatggttat tatgagaatg gaaaattttt ccatcacaca tcaggtgatg	1440
acagaactaa actatattgt gtagtataaa taagggtatg aaataccaac atcccagaat	1500
atcaacgagg atagaanggg anggagtttc aattanaata atcctgtnga ataaataaac	1560
ttcggntcc taaattcnnc taataccnac caaaccttag naccgtngta acanccctc	1620
caatcctcca ngggaaaaag aaaangtttt aataatttcc cnatccccga tt	1672

<210> 19
 <211> 690
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature
 <222> (1)..(690)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 19
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 aatatccac aatatatggt gctgcaaagt acgagtgttt acaagataga attatagata 120
 gccttcaatt ggccgaggag gaagaagatg acaccactga ctcaagtga gatgattcta 180
 gtgactcaga gagtgatgat gatgatagtg atagtggtag tgaaaccagt agtattggag 240
 acggttcagg tgaagataac gattctgatt cggcacccgga agagacatct ctgaaactac 300
 cacctttttc acagaaattc tttgaagcgt cagctgagcc aaaaccaata atagaagaga 360
 taggatctaa caagactgta gaagaaccat aacgaatgaa tataaaatac ttgtattatg 420
 tagtgccaat aaaagttgaa acggtcgac tacttttttag tcctgttggt ttgtgcacta 480
 ttttgtgtca gaaactgac tatgaaaatg atggttatta tgagaatgga aaacttttcc 540
 atcacacatc aggtgatgac agaactaaac tatattgtat agtataaata agggatatgaa 600
 ataccaacat ccagaatat taattatata gaanggaagg agtttaatat atatcctgtg 660
 gaataacaac ttcggtctaa ttcactatac 690

<210> 20
 <211> 1912
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<400> 20
 ctaggtttta attcactatc ataaagatca atggtttagcc caaaattaaa atatggaagc 60
 caaaacttcc gtggtcaaaa aatgaactaa gaagctaaag tctttttgaa acagtatgcc 120
 attatgtttt tcagatgttt ttacttgggt gttatattaa aatccaaagc tctgggtctt 180
 atcaagaatt tgtcagtcaa ctcatcatca aatgagtgga tatattactt tcaagaatca 240
 tcattaccaa gttgtcaaac gattgctaag caaatgttga agaatactga ttatttcagt 300
 tttgagaaac ctaaccccaa agataattta aggagaatca aaatttgaaa gaaaaggatg 360
 aaaagttgga gaaagaaacc ctattgaaaa tttaagtact gattgtttca gaaaatcatt 420
 gaatatgaaa caacagaaag gatattttac caactaatga acattttcct cccttataca 480

ccttaaaata cattaaatcc ttctggaata gttttttctc acaagacatt ttggtgtata	540
acattggtac tattgttgct gtcattgaca ataaggaatg ctacaaaacg tcaaggtaga	600
agctatcgat gttttttcca gctaattgaca ggacaacggt agaaacgaag tgtgcagacg	660
atttggttac aaagattgca agtgtatcaa ttatgctagc atatacctta ttttttcggt	720
gagagtatth ttatcatcgt tggctctgcaa aacttcaaag aaggggtgct atatgtgtta	780
aatgctgaga atcgaacact gtatctcatg gcgataaaat tcaaaatatt gtcgttagta	840
tgagaagatt ttgctgatat ttacttatat ttcacaatgt tcagtaaaga tccttatgac	900
ggtggtacaa tatgggacat gctatctgac acgttgacaa ccactaaaat cagctgttac	960
cgatagagac catacagatt gacgcaacac ataagtatac tcgaaaagct aaccacccat	1020
atcaggcatc aagccaaaaa tcaattttga ctgaaaatgg acgtcattaa ctctgagtcg	1080
ctaaaatcaa ggtatgaaat atttgccaaa gaggaaatcg atcagagtcg caatttctgt	1140
tcaatattca accaaataca attttccaac ctataaatct ccaccatctg tgttatgtgc	1200
tgtcattgag tttgcaactg atatttttgc tatatcttta cgttgcaaaa tatgcggggt	1260
gatgttaaac ttaccgaat tctccgtgta tcacatgtta ttatgccaaa tatgcatatc	1320
taggaaaaca gtctcaacca tctaacacac acattttctc accactgaag ctatgaagat	1380
agcccatctg ggaacggtaa acgacgtagc gggaaaaatg tgcttaaaag aatatgggaa	1440
aataaacggg tagacgtcat ttcccagtac catattctat tcagtcgaac gtcttcattc	1500
ttatcaacgg gggactggtc cagagacctt tcttatttta ttgtgattca gtagcgtcta	1560
ccatatacaa tgatattgta acttccgac aagtggaaac accgggagct tccaaagtat	1620
ggtatccgaa tataaagcca cccaaaatcc aattcaccac gagctaacac ctggggaaaa	1680
cgaggtgtct aaacctcctc aacttgattt cgagacttcg gtagtaggga agtttaaagg	1740
gcctattaca accacaaaag tggcaccacc accctccatg ggaggtctat taagtacatg	1800
gaaacgcag ctctggttga tacatcacct caatcaaaaa aattggtgtt ccacattcga	1860
aggaactaaa accgacgaga acctatcaca cgggtgctgac gatgataaga aa	1912

<210> 21

<211> 6140

<212> DNA

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature
 <222> (1)..(6140)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 21
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 atggcgacgc cacaacctga aatttggttc caactgttga ggatgattta tgtttgtgat 180
 tagaactaaa atcattcgag aaaaaaggaa taggagagaa ccaactttag tcgtgtaaaa 240
 agtaacatct gccattata aactatacgt agtccaaata atttacggta ttttctgtga 300
 ccccttcttg gcaatatcac aagaatatca taatgttcat gaaccctctt tgaacacgta 360
 gacaagtaaa cccaatgagg gggcagtgtt ctattcttgt aaactgcgca ccaaaaacgg 420
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<210> 22
 <211> 916
 <212> PRT
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<400> 22

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Gln	Glu	Asp	Leu	Thr	Ser	Met	Ile	Lys	Ala	Phe	Arg	Asp	Ser	Met	Glu
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Ala Lys Leu Asp Leu His Ser Gln Lys Leu Thr Ala Leu Val Ala Asn 35 40 45		
Ile Pro Arg Thr Asp Glu Gly Phe Glu Asp Leu Ser Gln Arg Ile Thr 50 55 60		
Val Leu Lys Asn His Gln Lys Ala Phe Leu Pro Lys Gln Glu Lys Glu 65 70 75 80		
Ile Gly Ser Leu Leu His Arg Gln Arg Glu Glu Glu Gly Asp Ile Lys 85 90 95		
Asp Phe Lys Thr Val Val Gly Glu Glu Lys Glu Glu Leu His Gln Val 100 105 110		
Glu Asp Phe Val Leu Lys Asp Gln Glu Glu Leu Arg Asn Val Glu Lys 115 120 125		
Lys Val Leu Lys Glu Glu Glu Glu Leu Gln Lys Val Glu Glu Ser Met 130 135 140		
Glu Lys Glu Lys Gln Glu Leu Tyr Gln Val Glu Asp Phe Ile Leu Gln 145 150 155 160		
Arg Asp Glu Thr Val Lys Lys Leu Gly Glu Ser Asn Gln Ser Gln Gln 165 170 175		
Glu Pro Tyr Thr Pro Ala Thr Ser Gly Ser Asp Gln Arg Phe Arg Ser 180 185 190		
Gln Gln Pro Asn Ile Gly Asn Thr Leu Ala Gln Asp Leu Ala Leu Ile 195 200 205		
Pro Lys Leu Asp Ser Glu Ile Cys Lys Ile Ala Val Lys Tyr Pro Lys 210 215 220		
Leu Phe Glu Thr Lys Leu Arg Pro Pro Pro Pro Arg Asp Phe Gln Tyr 225 230 235 240		
Lys Ile Gln Leu Thr Asp His Thr Gln Ile Tyr Ser Lys Pro Tyr Lys 245 250 255		
Cys Asn Gln Glu Glu Gln Ala Leu Ile Lys Asp Phe Ile Asn Glu Lys 260 265 270		
Leu Glu Ala Gly Val Leu Val Pro Ala Pro Ile Asp Ala Trp Leu His 275 280 285		
Pro Ile Phe Pro Ile Arg Lys Thr Asn Ala Asn Gln Ser Ser Thr Lys 290 295 300		
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Ile His Lys Asp Ser Ile Lys Tyr Phe Gly Ile Ser Thr Ser Glu Gly		
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Ile Phe Thr Asn Phe Val Arg Gln Ile Leu Glu Gly Ile Pro Cys Ile		
385	390	395
400		
Phe Ile Tyr Met Asp Asp Ile Leu Ile His Thr Lys Thr Leu His Asp		
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His Met Ser Leu Leu Arg Arg Ile Met Glu Lys Leu Asn Glu His Gln		
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Phe Gln Met Asn Tyr Asn Lys Met Gln Leu Leu Thr Thr Lys Ile Asn		
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Lys Ile Gln Ala Ile Gln Asn Trp Glu Leu Pro Thr Thr Thr Thr Gln		
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Ile Arg Ala Phe Val Asn Phe Ser Asn His Phe Arg Ile Phe Ile Pro		
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Glu Ile Ala Lys Phe Thr Asn Pro Leu Asn Glu Leu Leu Lys Asn Asn		
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Asn Gly Lys Asn Ile Lys Ile Glu His Thr Gln Ala Ser Ile Asp Gly		
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Tyr Lys Ala Leu Lys Ala Ala Ile Ile Gly Leu Pro Thr Leu Gln Leu		
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Ser Arg Tyr Ala Ala Met Glu Lys Glu Leu Leu Ala Ile Ile Val Ile		
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Leu Glu Lys Phe Arg Tyr His Cys Ser Asn Thr Val Glu Ile Tyr Thr		
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Asp Tyr Gln Ser Leu Ala Ser Tyr Leu Asp Lys Lys Thr Thr Pro Pro		

625	630	635	640
Pro Arg Ile Ala Arg Phe Leu Asp Leu Ile Gly Ser Phe Ser Pro Lys	645	650	655
Val Tyr Tyr Leu Ser Gly Lys Lys Asn Phe Val Ala Asp Ile Ile Thr	660	665	670
Arg Tyr Gln Thr Gln Asn Ile Lys Glu Leu Val Asp Glu Asp Lys Ile	675	680	685
Leu Gly Gln Thr Phe Thr Val Lys Arg Asn Leu Lys Gln Gln Leu Leu	690	695	700
Pro Arg Leu Glu Ala Ile Glu Leu Glu Asn Leu Asn Glu Ser Gln Val	705	710	715
His Lys Ile Gln Thr Ser Leu Glu Gln Gln Gln Gln His Asp Leu Glu	725	730	735
Asp Asn Asp Glu Glu Leu Pro Leu Gln Ser Phe Lys Leu Met Asn Asp	740	745	750
Glu Leu Phe Val Ile Ile Asn Asn Gln Leu Leu Lys Tyr Leu Pro Arg	755	760	765
Ser Glu Tyr Asn Asp Ile Cys Gln Thr Ile His Asp Lys His His Pro	770	775	780
Ser Thr Arg Val Thr Asp Tyr Leu Cys Thr Leu Ala Tyr Trp His Pro	785	790	795
Asp His Leu Leu Ile Ala Thr Asn Ile Thr Arg Lys Cys His Tyr Cys	805	810	815
Gln Leu Asn Thr Ser Ile Arg Glu Ala Ile Arg Pro Tyr Arg Pro Leu	820	825	830
Glu Pro Leu Lys Ala Phe Ser Arg Trp Gly Met Asp Tyr Ser Gly Pro	835	840	845
Tyr Phe Asn Thr Val Gln His Arg Tyr Ile Leu Val Ala Val Glu Tyr	850	855	860
Val Thr Gly Leu Thr Ile Ala Val Pro Thr Leu His Lys Asp Ala Asp	865	870	875
Asn Ala Ile Ser Leu Leu Gln Ser Ile Ile Ser Ile Met Ser Ala Pro	885	890	895
Thr Glu Leu Val Thr Asp Gln Gly Lys Lys Ile Phe Ile Thr Ser Phe	900	905	910
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<212> DNA
<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 23

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<210> 24
 <211> 748
 <212> PRT
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<400> 24

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 35 40 45
 Val Asn Leu Lys Met Met Lys Pro Phe Gly Ser Gln Val Tyr Val Lys
 50 55 60
 Ile Pro Ile Gly Val Lys Ser Phe Ser Ala Gln Ala Leu Ser Gly Ile
 65 70 75 80
 Met Val Gly Tyr Ala Thr Asn Lys Lys Gly Tyr Leu Val Tyr Asp Pro
 85 90 95
 Thr Gln Asn Arg Ile Phe Thr Ser Ser Gln Ile Ile Cys His Pro Ser
 100 105 110
 Ile Tyr Pro Ala Ala Asn Leu Thr Phe Asn Glu Pro Leu Ile Ile Ser
 115 120 125
 Ser Lys Val Thr Ala Ala His Leu His Pro Leu Thr Ile Ser Asn Leu
 130 135 140
 Val Ile Pro Pro Thr Asn Ala Val Ser Glu Thr Pro Leu Ala Asn Cys
 145 150 155 160
 Val Leu Ser Ser Asn Ser Ser Val Cys Pro Lys Val Cys Gln Leu Gln
 165 170 175
 Thr Val Leu Glu His Gly Glu Asp Lys Ile Tyr Ala Ser Ile Ile Pro
 180 185 190

Ile Ser Ile Gly Asn Met Lys Arg Thr Arg Thr Asn Glu Asn Lys Ile
 195 200 205
 Cys Gln Leu Asp Glu Ser Asn Asn Thr Thr Ile Pro Asp Ser Val Ile
 210 215 220
 Leu Ser Ala Asn Asn Val Leu Leu Asn Leu Glu Ser Arg Ser Ser Ile
 225 230 235 240
 Pro Lys Ser Tyr Lys Glu Ala Ile Thr Ser Asn Glu Lys Ser Lys Trp
 245 250 255
 Ala Asp Ala Met Asp Ser Glu Phe Asn Ser Leu Gln Ser Asn Asn Thr
 260 265 270
 Trp Ser Leu Glu Pro Leu Pro Glu Gly Arg Lys Ala Ile Gly Val Lys
 275 280 285
 Trp Val Tyr Thr Ile Lys Asp Thr Gly Arg Tyr Lys Ala Arg Leu Val
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 Ala Pro Val Ile Arg Gly Glu Ser Ile Lys Leu Ile Phe Ala Leu Ala
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 Tyr Glu Asp Lys Lys Arg Pro Asn His Val Cys Lys Leu Asn Arg Ser
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 Lys Phe Leu Gly Ile Asn Val Tyr Gln Gln Ala Asn Glu Ile Arg Leu
 465 470 475 480
 Ser Leu Asn Asp Tyr Ile Arg Arg Met Ile Glu Glu Leu Lys Leu Ser
 485 490 495

Val Ser Glu Thr Asn Pro Val Ser Ile Pro Ser Asp Val Asn Tyr Glu
 500 505 510
 Ile Phe Lys Val Asn Glu Asn Asp Asp Glu Lys Pro Cys Asp Gln Thr
 515 520 525
 Lys Tyr Arg Ser Leu Ile Gly Lys Leu Leu Phe Ala Ser Asn Thr Ile
 530 535 540
 Arg Phe Asp Ile Ala Tyr Ser Val Asn Ser Leu Ser Arg Phe Ile Asn
 545 550 555 560
 Asp Pro Lys Glu Lys His Trp Ile Ala Ala Val Lys Val Val Lys Tyr
 565 570 575
 Leu Ser Gly Thr Gln Arg Tyr Gly Ile Cys Tyr Asn Gly Asn Gly Asp
 580 585 590
 Leu Asn Ile Tyr Ala Asp Ser Asp Trp Ala Ser Thr Pro Ser Asp Arg
 595 600 605
 Lys Ser Ile Thr Gly Tyr Ile Val Thr Tyr Ala Gly Ala Pro Ile Ser
 610 615 620
 Trp Arg Ser Lys Lys Gln Asn Val Ile Ala Leu Ser Thr Thr Glu Ala
 625 630 635 640
 Glu Phe Met Ala Leu Thr Glu Ser Ile Lys Glu Ala Leu Trp Leu Ile
 645 650 655
 Tyr Ile Phe Arg Asp Ile Asn Val Ile Leu Lys Leu Pro Ile Val Ile
 660 665 670
 Tyr Glu Asp Asn Leu Ser Cys Gln Lys Leu Leu Glu Asn Pro Arg Phe
 675 680 685
 His Asn Arg Thr Lys His Ile Asp Leu Lys Tyr Lys Phe Thr Lys Asp
 690 695 700
 His Ile Glu Ala Gly Thr Ile Lys Val Glu Ser Thr Asn Ser Ala Asp
 705 710 715 720
 Asn Leu Ala Asp Met Leu Thr Lys Pro Leu Pro Lys Ile Lys Phe Lys
 725 730 735
 His Leu Arg Trp Leu Ala Gly Leu Arg Pro Leu Asp
 740 745

<210> 25
 <211> 1550
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<220>

<221> misc_feature
<222> (1)..(1550)
<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

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ctttctttgt tttgttttgt ttaccttggtg ataattttat acgtgttgag agggctctcg 180
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cgcaccgtac ggtaatgata tctgattggtt gttggagcgt tcttcgctaa caggttcttt 300
ctttttgttc aggggtttcg aaagataatg tagaaacacc agggcttata actgagagtt 360
agagtagtgg agattagtag tagtagtaca atcctatagc ccaaacatta ttggagagat 420
cttaccaaat agcaatcatc atgatgtatt tactactaca taaatnattt aagacgacat 480
ttaccagcaa taaacaacat gaccaactaa ttaacaaaca tttgaaaaac ataaagtaat 540
tagaaagttt aaaaagtgtg caaccagtgt ggaaaaagaa tggaattgga attgaacaaa 600
gttattaatt actgaaaaag gaaatttaat ttcttgaaag gcaaattctt gtttgttttt 660
ttttttgggt cttttctttc atttaataag cgtgggggtat taatagataa tgatattggt 720
gttggttattg tgatattggt gtgaaatttg acatatgata agataagttt ctttcttttc 780
tttcaactag tataattgaa ctaaagacca ccaccaccac caccacatag ttagcaacct 840
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taatgctaatt tcttgattag tgtggaaagc ctaataaggt tatattgtgc acagggttaac 960
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attaaagtgt taggttgagt taattgatta gtgaaaacca actaactacc gtattaaatt 1080
attgtattaa gattgattcc tattaaggat aaaacagaga gtgtgttaga aagagaaagg 1140
gtggattata aatatgtgta aaatccccct tagagactaa ccactagaaa tctattgatg 1200
gtttcatata tagagattaa cgattatatt tataatataa gttggtagtt gctagtatat 1260
ntgaaagcac tacagtatag tatgtcagaa tcagatcatt taaactctac taataataca 1320
ggaaacactt tcattagtct agatcaagcc agtacaataa tggcagatca aactcaagga 1380
gctaaccac aacaatgata attcatcttt tttgtcaaga cgatagttaa tgttacaagc 1440
acttttnattg ggctcgaaat agtggtaaatt agggccata ggatatgacc tgttacaagt 1500
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<210> 26
<211> 2132
<212> DNA
<213> Unknown

<220>
<223> sequence of retrotransposon from unknown organism

<220>
<221> misc_feature
<222> (1)..(2132)
<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 26
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tattgctgat agatgttgaa aaaaaaacgg aagaatgggg atagcaaaac tgtgggtgag 180
attaactcat ctatggcgct aaaagtcttt tttttttctc ttttattagg gggcacataa 240
attattcttt tcattgataa tcccgagtcg gttttttggt cattattcgg aatatattac 300
cgtattggga acgataatta ttattagttc tccccgatgg ttcgattttg ctggtgcaaa 360
aatataaatc cgatataact ttattggtgc ttgataaat ccgttttata agttggtaga 420
catatacagg atgataataa tttaacggat ttataagttg gaatcatttg gatgaatccg 480
cttggggagg cgttttccaa ttttagaagt ttaactatca attttatgtg acatccgagt 540
atacacattt tgtgaatttg atcttgtaaa ctcaactggt gtaccatggc atttataaca 600
acactttcta gaatcggctg agttacatgc atttcctcta tttgtagatt aatggaaatt 660
catgaaatcg ttcacatttt tttctataat gagtatcggt cggtttccat aagtagggga 720
ctaaaaaata attgatatct ctaatcagtg acagctctag tcaacttgac cgtaatgttt 780
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tcaattcccg tcaaaacgca tttggcactt aatctttgat tgaaccgatt ttgatctcaa 900
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gaattaatac gagaatatca aattatctta gagaggggtct cacagagcaa ctttctgagg 1140
cacacggtca ccaacatgat ttgttataaa aaattcaacc aaattttgga aaaaatgaaa 1200

acaaaacaaa acaaaatctg aaacatcccg aaagtcacaa atgcttgatt acttaaaatt	1260
acttatttgc ttcaagacgc tattattatt attatgacat aatactactt gaataacagt	1320
gaactgtaat tgtattaaga acaaatcata acaaaggaag atgatgacga tgatgatgac	1380
cccttgaaat atcccagggc acatgcattg tgatgattgt tgtaatatag ctaatgctaa	1440
ttcttgatta gtgtggaaag cctaataagg ttatattgtg cacagggttaa ctaccttaat	1500
atagttattg ttaatacagt tattgctgtt gactactatt gttattgtta aattaaagtg	1560
ttaggttgag ttaattgatt agtgaaaacc aactaactac cgtattaaat tattgtatta	1620
agattgattc ctattaagga taaaacagag agtgtggttag aaagagaaag ggtggattat	1680
aaatatgtgt aaaaatcccc tttagagact aatcactaga aatctattga tggtttcata	1740
tatagagatt aacgattata ttataatat aagttggttag ttgctagtat atttgaaagc	1800
actacagtat agtatgtcag aatcagatca tttaaactct actaataata caggaaacac	1860
tttcattagt ctagatcaag ccagtacaat aatggcagat caaactcaag gagctaaccc	1920
acaacaatta ccatattata tgaagaagac tataacaaaa ctgtagatag taggggattg	1980
ggatatttccg ggggagtaga agtattgggg ttatctaagt ccattcttaa ccaccaaca	2040
atccaacaac aaccaacna cgtttttccc caattctcng gagatnactt gattaacttn	2100
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<210> 27
 <211> 1734
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 27

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aacaccgttt gttgaagatg gctttatccg tatactattg ggcgtcgatt ttcgcacaaa	180
agcttttatc cacggaatat ttgcgataat atagtacaaa agtgtgttct agtcttgtaa	240
atgtccaata ttttttagtac aacgatggaa acccgatatag cgcagacaca gtttggatag	300
atttacgtag gtgatgagga gttaaattga atattcttgt ataatttcaa gagctgtgac	360
tactatttaa attttttcca cttcactttc tttctcttct ttgacattca agttagtctt	420
tctgtatttg aataatacta catttatcat gtctcacgtc tcaattgtaa ctggtgcttc	480

tagagggtacg ttttaatgaa caaaatctat gatgttgaga cttccaattt gaacttttagt	540
actaactcaa ataaaggcat tggtaaggct atcgccgaaa ttctttttaa aactccatct	600
tcaaaagttg tgattgttgc tagatctcaa gctccattgg aatctttcca aaagcaacac	660
ggctcggaca gagtagcatt tgttgctggg gatattacag atccagcaac gtctaagact	720
gctgttgaaa ctgccatctc caaatttggg caattaaatg ctgtcatgtt gtaatatagc	780
taatgctaata tcttgattag tgtggaaagc ctaataagggt tatattgtgc acagggttaac	840
taccttaata tagttattgt taatacagtt attgctgttg actactattg ttattgttaa	900
attaaagtgtagt taggttgagt taattgatta gtgaaaacca actaactacc gtattaaatt	960
attgtattaa gattgattcc tattaaggat aaaacagaga gtgtgttaga aagagaaagg	1020
gtggattata aatatgtgta aaatccccct tagagactaa tcactagaaa tctattgatg	1080
gtttcatata tagagtttaa cgattatatt tataatataa gttggtagt gctagtatat	1140
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aattttcaac acttgatcac aagtgcggggg attaatacata attgcaaaga gtgtgttaga	1560
aagagcgaag gtggattatg aatattggag aatcctcttt agagactatc cgctaacaaa	1620
atagatgaac ttgctcaaca gaaacaacta atcgactaac tgactaaaat taatatacta	1680
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<210> 28
 <211> 5734
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature
 <222> (1)..(5734)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 28

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ttaaaaatta accagctctc aaataacaaa agtttaaatt ttcaaggttt gtaaacaatgg	180
cagctagtag taggatgggt cataatatta attaattatt agtaataatg gctaagtttt	240
tgaagcattg ttttaaattt tcaaattgaa attcaatttc attacaaatg gattactaac	300
ggaattccta agctcaactg aataccgtga ttgaaacatt tgaatttgta tcttttagat	360
tagctatttt tacttttttt gtcattgtag ttggttatga taattacaag aaactaaagt	420
ttaatatattt aatattcatt ttcttttttg gccaaactgc aaataacaca caaacccaaa	480
attaaataat tagatttaat gcatgcataa ttacacagaa tgtttagcct taacaagtat	540
tctagaaaca agaaagaaaa aatgtcgtct tggcgtttat ctttaattgta ttctgtaaac	600
tgggttaatt cttatttcca acttttcatt tttttggatc ttgtatggaa taaaaattaa	660
atatggtatg ttttaggggt gtattaacaa tacttacaat tatcaatcat acagctttac	720
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tctattcata tgcattacac atttagtttc tattacaaat agtgatgcaa tggtgcaaga	1020
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ttattatatt cagtcgtgag tgtaagctat ttcgttaggg ttatcttaac tcgaagttaa	1140
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gtggggagga aatccattaa tgattataaa atgaaactct tggtaacctt attgaaacac	1260
cacattcagt acattttcaa ccgtcactat tattattgtg gcaaattgat taaacaatag	1320
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aacaccagat gtattacagc tttaaacttt gtttctaatt tgaccacaaa aagttgtctg	3240
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<210> 29
 <211> 1875
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
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 <222> (1)..(1875)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

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gacgaaagtt tactttacac aaggggagac catatgtctt ctttattaac aactagttat	420
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attgttaata cagttattgc tgttgactac tattgttatt gttaaattaa agtggttaggt	960
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attcctatta aggataaaac agagagtgtg ttagaaagag aaagggtgga ttataaatac	1080
gtgtaaaatc ccttttagag actaaccact agaaatctat tgatggtttc atagatagag	1140
attaacgatt atatttataa tataagttgg tagttgctag tatatttgaa agcactacag	1200
tatagtatgt cagaatcaga tcatttaaata tctactaata atacaggaaa cactttcatt	1260
agtctagatc aagccagtac aataatggca gatcaaactc aaggagctaa cccacaacac	1320
gtcttcttca gtattagga acaacatact aacttgacct tttctagctt caaccaaaaa	1380
ttcctctata tccattaatg gaatttcac aaactgagca gccccaaaaa acgttttgct	1440
tccaaagtct aaatgagcat ggaatttcct tatgaaaggt ataccaagta ttaatttctt	1500
atggaagctg tccactacag caaaattctc ttggaatgta ataccattaa actggaactt	1560
gaggttaatt atttggttaa agtttctggt gatttttggt ccaataaagt acccaaacta	1620
ctagagctcc aacaacattt tcagaaaatg gccaaataa caataagtgg gtatatttta	1680
tcaaaagagt ttatattatg gttactcgac ggggtattatt ctctggtgga ttaaggcatc	1740
tgggcgaccc agtgggacca aaattccaga gtagtggttt gggttaggac tttaccaagg	1800
nccatgatta gggaatattn taaccaaaaa attaaaatta ccatttaatt cnaaaaccta	1860
acctaaattc cctaa	1875

<210> 30
 <211> 1712
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature

<222> (1)..(1712)

<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 30

taaccatgga attcctngaa ttantnataa ttaaccaaatt tttttagggg ttattaggac	60
ctaggattga attccatggt tatttaataa ttaancccca gtttggccaa ctatgaaata	120
gtataatggt taaatgcaaa ataaatatag tatgaacaat atgatagttt tagtgtgaat	180
tttgaataag aaaaagaagg gataaggata tttttactag gaaactcaat tataattact	240
aatgataaaa actccatcag ctactattat tactcaaatt ttaaatacatt tgtttatcac	300
ctacacaaac agggattgtc caatattgat tactaaaatt agaacaata agagaatata	360
attgaagtta aataattcct ttactaaatc tattgaccaa gaactacatc aagggaagt	420
gttgcataata catctaattg ttattcttgg ttagagtatt gatacaaaat tatatcatca	480
ccaacgaatc acattaaggg aaagtgttgt gcatatacct gatgcttagt cttgggttaa	540
gtatttgtgt gaaagggttat cgtgaccaa gattatagta agggaaagta ttatgaataa	600
atccaatgtc tactttttaca gaagtattga catgagagat tataactatc aagaattgca	660
ttaagggaaa gtgttgtaat atagctaatt ctaattcttg attagtgtgg aaagccta	720
aaggttatat tgtgcacagg ttaactacct taatatagtt attgttaata cagttattgc	780
tgttgactac tattgttatt gttaaattaa agtggttagt tgagttaatt gattagtga	840
aaccaactaa ctaccgtatt aaattattgt attaagattg attcctatta aggataaac	900
agagagtgtg ttagaaagag aaagggtgga ttataaatat gtgtaaaatc cccttagag	960
actaaccact agaatctat tgatgggttc atatatagag attaacgatt atatttataa	1020
tataagttgg tagttgctag tatatttgaa agcactacag tatagtatgt cagaatcaga	1080
tcaattaaac tctactaata atacaggaaa cactttcatt agtctagatc aagccagtac	1140
aataatggca gatcaaactc aaggaggtaa ccactacag gttatgagcc tcgcccgtt	1200
attgaattta gataatatag gggcaatgaa agcttttgaa agtggtgatt ttctgaatc	1260
attaaaaacta gaatccaaga ttaattttca agtggtgaga aatgaaatcc ttagatatgc	1320
acgtggtatt ggtgctgagt ttgaaaactt tgtattgaat gaaactccag ctcacctgta	1380
tgatcttaga ttgggaaata tgcttcatca attattgatt cgcactgtga aagaaaaagt	1440
tagaatgcct aggcaagaac ttggaaaatc aggaaaagaa ctttatcttg atcttattaa	1500
atcattcggg actcaatacc catacgataa atttgagata gttaaatact attgggatca	1560

gttaacaaac cctttaatta atgtgaagag acgttttgaa attgaagaag tatgggttca 1620
 atacattaat gctcaaactg caacagagag agaagttctt aattcatttg tttggttaca 1680
 tttgtcaaaa tctatattac cacaagagta cc 1712

<210> 31
 <211> 1540
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature
 <222> (1)..(1540)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 31
 tgtggaatta agatgacttt gtgattaaat tgttgacttc ttaagcctt ttaatgtgga 60
 ggaaaaagaa aaatctataa ttaaaaaaaaa aaaagataaa gcagataatt ctttgatctt 120
 tatatacttg gtctatatgt agtaggggaa agtcggagtc ggaatttgaa aaaaaagag 180
 aaaaaagaac gaatatttag actgtaaaat tcaaaccctt gctgattagt atataaaaaa 240
 aatgagttca tttttccttt cttttttttt ttttcgcgcg gatagcaacg gtcattaagt 300
 taacgagata aaaaagaaac aaccagataa ttatgaaaag ttgtgatggt gtcacgtgcg 360
 aacatgagag tcatgaattt tgacgaaaac gtcaagcttc agtttacaaa agacctcttt 420
 attaaaatcg aattgcttat agggtcgctg atgatgagaa ggtgtatggt gtaatatagc 480
 taatgctaatt tcttgattag tgtggaaagc ctaataaggt tatattgtgc acaggttaac 540
 taccttaata tagttattgt taatacagtt attgctgttg actactattg ttattgttaa 600
 attaaagtgt taggttgagt taattgatta gtgaaaacca actaactacc gtattaaatt 660
 attgtattaa gattgattcc tattaaggat aaaacagaga gtgtgttaga aagagaaagg 720
 gtggattata aatatgtgta aaatcccctt tagagactaa ccactagaaa tctattgatg 780
 gtttcatata tagagattaa agattatatt cataatataa gttggtagtt gctagtatat 840
 ttgaaagcac tacagtatag tatgtcagaa tcagatcaat taaactctac taataataca 900
 ggaaacactt tcattagtct agatcaagcc agtacaataa tagcagatca aactcaagga 960
 ggtaaccac aacatagaat acgttttcaa ctacttaagt atccactaac ctaaattttt 1020
 tttttaataa aatttcattg tattagtctt tcttactgct tttaatcaac tataagtata 1080

ggtttccggtt ttttttgcag taaaatttat cgttcaggag aaataacaaa atgtacacga 1140
 cttattcgca gcattttttt ttttgtttg ggtttttgta tcaaattggtt acaacaacaa 1200
 caacaacctc aattcttaac caaatctacc cctcctattt tttttncnca tacacacaat 1260
 acatcttaca ctatcttttg ataggcttta tngaagangt atttangng tgtaatgaca 1320
 atctgcttaa cncatatatn tatntanngn nngtngtcaa caatagcttt atctactttt 1380
 tttttttggn nacnccngna acttcaggnc cacnnntttg ccnattttgg ggcccnatt 1440
 nggaaaacat ggggnattggg annacagctt tttttagggn naaangggtn ttncnttttn 1500
 tgggtgggctt ggaaagnaac agcntntaaa nnaatgggct 1540

<210> 32
 <211> 2025
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature
 <222> (1)..(2025)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<220>
 <221> misc_feature
 <222> (1)..(2025)
 <223> sequence of retrotransposon from unknown organism

<400> 32
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 ggattgacga agcattatat attcgtctaa aaaccatttt tgctgggttc gcaataaatc 120
 tcggagatta tttctcgatt accaatttat gttgttttgt gacatttctt atattttgtt 180
 ctattttaca cgactattta ttgttaataa atatgtcacc taaagaatat ttctatttag 240
 ttttacatat gttttttgac gacaatcaac tattacaaat taacctacat tttttaattt 300
 gaatatatac aatttatatt gaattaacat taccatttag tttttgataa gaatagattg 360
 cgctatttca aacatttggtt aaattattta ttgtgaaaca actatgtaga ataaaagtat 420
 gaacaaatc tacgttcac atgtgggggtg tgccttcata tatatctttg gatgagaatg 480
 ccaagaaaaa tgatggcgtg acaattcaat acggcaaac aaactaatcc cctctaagat 540

tttactagtg tgtttcccta tegtctgagg aaaaggtaac aaaacatcgt ttaaccaatt	600
ggtgtttgtt acgatgggtga cgttgagtag tgcatatagt tgcaacggca aattgcatcc	660
agcgagttaa cagcgaatgg caaagtgaag cctccgactt gtgttcattg actactggga	720
ttggactggg aataacgact taactaatta atgttctcgt ggactcgttt agctagaact	780
aacatttgtt ataatatagc taatgctaata tcttgattag tgtggaaagc ctaataaggt	840
tatattgcgc acagggttaac tcccttaata tagttattgt taanncagtt attgttggtg	900
actactattg ttattgttaa attaaagtgt taggggttagt taattgatta gtgaaaacca	960
actaactacc gtattaaatt attgtattaa gattgattcc tattaaggat aaaacagaga	1020
gtgtgttaga aagagaaagg gtggattata aatatgtgta aaatcccctt tagagactaa	1080
ccactagaaa tctattgatg gtttcatata tagagattaa cgattatatt tataatataa	1140
gttggtagtt gctagtatat ttgaaagcac tacagtatag tatgtcagaa tcagattatt	1200
taaactctac taataataca ggaaacactt tcattagtct agatcaagcc agtacaataa	1260
tggcagatca aactcaagga gctaaccac aacagcattg attatataat catctatgta	1320
gccaatatac actaccgtcc aaactccac tacacacttg taacagtgtt ttacaaatct	1380
atgaacgaat aaccgattca aatgacacaa taaagaacat ttcaccgatt tgaattgcta	1440
atcggtagta taatattgat ggaagggttaa gagtttaatg ctaccctagg tttaccggag	1500
atcaacagtt gcatatacaa aacgtgttat ctgtctacga atggccttct atgtgtataa	1560
aatgtttcat caattgataa ttaattatta atctgcttac tgaggtaaac cccttttaat	1620
gcaatagcaa atatgaggta tttttttgct attgacatgc gtatatgaat ccatttgtat	1680
caaattgccg atataatgaa atggaaatta agggaaaaaa aaaagtttat atccaaattc	1740
atgcgattaa caggttcttg tgattataat tggttaacccc ctcccccta aaactcatat	1800
ctgccaaaag aggaggatat ttgaatatgc tattatgaac ccattgatt ttgactacaa	1860
ttggatttgt cgggtattga aacccaaaca tattataatt tgctatgcgt ttaaatcaac	1920
cgtttactgg tagatcctat actataaata cagccaacaa tcccccaattg ttcagataaa	1980
gtaacactca atatcatttg atcaatcaat caagaggatt acaaa	2025

<210> 33
 <211> 3583
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<220>

<221> misc_feature

<222> (1)..(3583)

<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 33

aaaannttcc ccatngccta ttcctaggnc ccaaaaccag ttgtccgaaa ctccatggat	60
gccagaagtg gtggtcctcc gccgttatgg ttggaaaaga aaaagaaact tgacgaattg	120
aaagtcaaag aagagcggca agaaagaagg aagaaggggc aaagaaaaag gaagaagagg	180
caaagaaaaa ggcagaggaa gcgaagaagt gttttatttt acttttctgt caaatTTgca	240
ctacttttaa tttgtgtgca aatattctat tttacttgat ttttatatac ttttatttta	300
caatactttt ttataggact ttttatatct tttctttatc aactgttcgc tatagggtag	360
gtcttccaag ctaatTTTtac ccgacacaag atgaaatatt ttctgttgag cactcgttgt	420
cgacagtga aatTTTtcac tcaagaaaat attttatcat cactTTTTct agaagggagg	480
ttcaagtgtt ggagaataga cagcgaacac ctgatattcc caaggTCgaa ttagattgaa	540
agataaataa tagtcatatt tattttgtat ttagtcaata aattatcttt ttatatttaa	600
attcttagta ttgtcatacc acgtagattg atacggacat acttagcaca tttaacatat	660
attaagcacc gattacctgt gacattccgg agtttactgt ttcgcgcacg ctggcagacg	720
aacatcaact catcttttat acaatatatt cttacgatta taactttcaa ttaagaaata	780
caacttctta ttagcattct cctacaagtt cttaagttcc taggaatttc ttcgaaacta	840
taattaaaga cggaaaagtg taaaacaaac agaaagcaga ggaggccaag aagaaagcag	900
aggaggccgc cccacaaaag tttgacaact ttgacgactt tattggcttt gacatcaacg	960
acaataccaa cgacgaagac atgttgtcca acatggacta cgaggaccta aaattggacg	1020
acaaagtacc tgccaccaca gacaacaact tggacatgaa caacatactt gaaaacgacg	1080
agctgatact agacgggttg aacatgacat tgctcgacaa tggcgaccac gtaaacgaag	1140
agtttgatgt agacagcttt ttaaaccagt ttggtaatta ggggctctgt tctacaagac	1200
atatacagat agtgcaggaa taagaaaaga aatattttat atagctatat atttcaagtg	1260
tttattctgt tcaacaagtt ctaaccgtag atacacaaa tcaccaagtc agacattact	1320
gagctagctt aacggTccaa ctactttaaa ttgcaatccg ttctttactt gagtcagtcg	1380
actctacaac aactatcctg aggtgattat tttttggtgg aaattttgac caaattctta	1440

agcaaaaatc tagtttctac tgataaataa atacacattg ctctacttct gtactccaca	1500
ctctgctatt gcttgatagc catccttaaa tcaacagaat ccactaatc tgctacttcc	1560
agaaccatga ctactctaca tttttaacca tctcaattaa ttaccatctt tttctctcat	1620
tatttggcac tatggccgag ttggtctaag gcggtagact caagaattat tcttctctg	1680
cgatccaggg gtttctacta tcgtaagatg caggagtctg aatctccttg gtgtcattat	1740
ttttttttt ccaagaacct ctcatTTTTT tttttcaaaa attatttcta caatttcctc	1800
tattcttaaa aatctttggt attaaactaa aaatgtacct aactaaacta ctaggctgga	1860
aaataataaa tctaacgta acgaaataag caaaagtaat tttttttttt caagacaatt	1920
ccatgtttgg ggatgaaaac tgccctgcaat tatatatcct gtaacaatcc ccttatatca	1980
acaacaaccc gagaacaaca aaaagtccac tggcagaaac cttaccacca atattctcaa	2040
tttgtgtcac tgattgggca gtttgtgtcg atatccatga tgtggtcaaa ctggcagcag	2100
tggtagatgg ataaacactt tcagcagcaa cagtaaccga gttgacaact tccttagcag	2160
cttgtgtatc acactcttca tcatcatccc agctatcatc ctcatcgtca cactctgggt	2220
caggagtttg atcatcttca tcatcgtagc catcttcacc agggcaaaca taatcgttac	2280
cagatccacc ccaccagctt ccagacgatc caccagtaac tgaagaagaa ccggaatcac	2340
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cccaccaaga gcctgtgcca gatccagaac ttgatccacc tgttggcaca cattcgccat	2460
catcttcttc ataccattcc cattcaccat catcagagga gccactggca gaaccaccgg	2520
cattgtcttc cccttcatag ccatcatctt ccagtcac tggtatagaca gtgtgtgtgg	2580
taataacagt cacagtcgtg gtatatagct gtccacctgg agcaacagtt gtcagtggac	2640
atgtggttgt gattgtcaac gtaacagttt catcacagat ttcaccagat tgtgtgagat	2700
aagtggtaaa tgtctgacca ccaccagtat atgtgataga aacaacttcc gtttcagtat	2760
gttgattagt ggttggaggt aattttgtgg tgagtgtttg agttgttggc accccatcgg	2820
aagtaaatgt tctagtgggt gacacagttg gatggatagt aggaatttca gtttcacaat	2880
cagtctcgtc atcgtcgtca tcagaagtgg ttgactttgt tgggagaaca gtaatagatc	2940
ctgaccaggt tggaataata gttggaagaa cagacgttgt tggaagaact gaccacttg	3000
gaatgatggg tggaacgtct gtctcacaat cagtctcaat tatcttctgt agtggctttt	3060
tgaaacaact gacgagacac ttgtcttact ttgactggtg attggaaggg ttggaattgt	3120
aggacaaaaa tttggggcct ccattggatc tttacactct ccaccactgc acaactttaa	3180

tttggaaacca caactggaac tagtttctgt ttcaaggctt taccagttga cctgatcgta	3240
ataagccacg gggttaccaa cttgttgcac cttcactgat cagccatcaa tctttgataa	3300
gccctgattt ctctcatcta tgcaacaatc ttctattgtg aatcatttgt tttgctaaac	3360
ttgtagttgg tgtccaaaaa aaaaagtgat gtaaaattta aatttttctg aacttgctgt	3420
gtaaaaaagt ctccagaaaa agggacaaca cacacaccaa tttttcacca taccacacaa	3480
ttcaccaata agctctctca tatccatcna ataattacag tacagcctcc tattencaat	3540
ttttggnatt taaaccagtt cccttggcag gtcaccagtt cat	3583

<210> 34
 <211> 770
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<400> 34	
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ggataatcaa gcggtcatta caatcttaaa gaatgataat ttccaccacac atagaccgat	120
tgatatatgt taaaaatttc tcagacaaaa attgaaagat ggattttttt caatatcata	180
tgttgaatct ggagataatt tagctgactc attcacgaaa gctttaggaa gaaataaatt	240
gattgaacat accaaaagga ttagagaaaag aaaggattat gataataatg ctacactgat	300
agtggacgtt aggacgctcg aagagattaa gataaacaag aaattggtac atcattaatt	360
aatttagctg ttacctgaa tcaggggagt gttcgctata gggtaggtct tccaagctaa	420
ttttaccga cacaagatga aatattttct gttgagcact cgttgctgac agtgaaaaat	480
tttcactcaa gaaaatattt tatcatcact ttttctagaa tggagggttca agtgttgag	540
aatagacagc gaacacctga tattoccaaag gtcgaattag attgaaagat aaataatagt	600
catatttatt ttgtatttag tcaataaatt atctttttat atttaaattc ttagtattgt	660
cataccacgt agattgatac ggacatactt agcacattta acatatatta agcaccgatt	720
acctgtgaca ttccggagtt tactgtttcg cgcacgctgg cagacgaaca	770

<210> 35
 <211> 106
 <212> PRT
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 35

Asp Leu Arg Asn Thr Ile Glu Asp Leu Glu Leu Lys Ile Arg Asn Leu
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His Val His Glu Asp Asn Gln Ala Val Ile Thr Ile Leu Lys Asn Asp
20 25 30
Asn Phe His Pro His Arg Pro Ile Asp Ile Cys Tyr Lys Phe Leu Arg
35 40 45
Gln Lys Leu Lys Asp Gly Phe Phe Ser Ile Ser Tyr Val Glu Ser Gly
50 55 60
Asp Asn Leu Ala Asp Ser Phe Thr Lys Ala Leu Gly Arg Asn Lys Leu
65 70 75 80
Ile Glu His Thr Lys Arg Ile Arg Glu Arg Lys Asp Tyr Asp Asn Asn
85 90 95
Ala Thr Ser Ile Val Asp Val Arg Thr Leu
100 105

<210> 36

<211> 598

<212> DNA

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 36

cttcaatgct tcacttgtag tagtaccat gattgtatag tgggtgtggtt gatcgacttc 60
aatataacaa gagagagatg agatgagatg cttttatcgc gtatatatatt ttttttccat 120
tgacaattct gatttcacaa attgttcgct atagggtagg tcttccaagc taattttacc 180
cgacacaaga tgaaatattt tctggtgagc actcgttgtc gacagtgaag aattttcact 240
caagaaaata ttttatcatc actttttcta gaatggaggt tcaagtgttg gagaatagac 300
agcgaacacc tgatattccc aagggtcgaat tagattgaaa gataaataat agtcatattt 360
attttgtatt tagtcaataa attatctttt tatatttaaa ttcttagtat tgtcatacca 420
cgtagattga tacggacata cttagcacat ttaacatata ttaagcaccg attacctgtg 480
acattccgga gtttactgtt tcgcgcacgc tggcagacga acagattaga agcttggtaa 540
atctttgggtt attcatcacg tcttgagaat aatacaaagt ttaatatagt attttcaa 598

<210> 37

<211> 1082
<212> DNA
<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 37

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gagctctaga acaacccccc actcactagc catcgccaca ccaacaacca aattgctgat      120
ccagaaaaaa taccaccccc gtagtcgggc ttgtatggaa taattgcttg gccaggtacg      180
tccccacctc atcgtgtctt ttctggttga aatatgtcat ctcccgggct aacagtaccg      240
tatctctgtg gctggggcat ctatactctt tcattctcgg cttacaaatc tatcttgttc      300
acacatttca tatactctggg acttgctgaa ctctctgcac tctatcataa actggaactc      360
gcttgcatte tgggacacac actggagctg gaatccatgg tcaggaaatg tgaaaatttt      420
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aacacctgat attcccaagg tcgaattaga ttgaaagata aataatagtc atatttattt      780
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cgcatcagtt tcctctgggt tctctttttg atcttggtga actacctttt tttcccactc     1020
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tg                                                                                   1082
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<210> 38
<211> 39
<212> RNA
<213> Candida albicans

<220>

<221> primer_bind

<222> (11)..(21)

<223> minus strand primer binding site

<400> 38
gcucgcgugg cguaauggca acgcgucuga cuucuaauc

39

<210> 39
<211> 71
<212> RNA
<213> Candida albicans

<400> 39
uauuccauca gauuagaagu cgauagugau aaucuuuucg ucccaaauua gcguuguaua
aaucagucc u

60

71

<210> 40
<211> 11
<212> DNA
<213> Candida albicans

<400> 40
gaatcaggga g

11

<210> 41
<211> 11
<212> DNA
<213> Candida albicans

<400> 41
aatcagggga g

11

<210> 42
<211> 11
<212> DNA
<213> Candida albicans

<400> 42
atccagggga g

11

<210> 43
<211> 14
<212> PRT
<213> Unknown

<220>
<223> protease sequence of 1731 retrotransposon

<400> 43

Thr Gln Trp Cys Leu Asp Ser Gly Ala Thr Ser His Met Cys
1 5 10

<210> 44

<211> 14
<212> PRT
<213> Unknown

<220>

<223> protease sequence of copia retrotransposon

<400> 44

Cys Gly Phe Val Leu Asp Ser Gly Ala Ser Asp His Leu Ile
1 5 10

<210> 45
<211> 14
<212> PRT
<213> Unknown

<220>

<223> protease sequence of Tnl retrotransposon

<400> 45

Ser Glu Trp Val Val Asp Thr Ala Ala Ser His His Ala Thr
1 5 10

<210> 46
<211> 14
<212> PRT
<213> Unknown

<220>

<223> protease sequence of Ty1 retrotransposon

<400> 46

Gly His Leu Leu Leu Asp Ser Gly Ala Ser Arg Thr Leu Ile
1 5 10

<210> 47
<211> 14
<212> PRT
<213> Unknown

<220>

<223> protease sequence of Ty4 retrotransposon

<400> 47

Lys Leu Val Ile Ile Asp Thr Gly Ser Gly Val Asn Ile Thr
1 5 10

<210> 48
<211> 14
<212> PRT
<213> Candida albicans

<220>

<221> UNSURE
<222> (1)..(14)
<223> protease sequence of pCal retrotransposon

<400> 48

Lys Tyr Leu Val Tyr Asp Thr Gly Ala Thr Ile Ser Val Val
1 5 10

<210> 49
<211> 63
<212> PRT
<213> Unknown

<220>
<223> integrase of retrotransposon 1731

<400> 49

His Lys Arg Asn Gly His Cys Lys Thr Cys Lys Ile Lys Cys Ile Arg
1 5 10 15

Ser Asp Asn Gly Gly Glu Phe Val Asn Asn Val Phe Asp Asp Tyr Leu
20 25 30

Lys Ala His Gly Ile Ala Arg Gln Leu Thr Ile Pro His Thr Pro Gln
35 40 45

Gln Asn Gly Val Ala Glu Arg Ala Asn Arg Thr Leu Val Glu Met
50 55 60

<210> 50
<211> 63
<212> PRT
<213> Unknown

<220>
<223> Integrase sequence of copia retrotransposon

<400> 50

His Glu Arg Phe Gly His Cys Glu Pro Cys Lys Val Val Tyr Leu Tyr
1 5 10 15

Ile Asp Asn Gly Arg Glu Tyr Leu Ser Asn Glu Met Arg Gln Phe Cys
20 25 30

Val Lys Lys Gly Ile Ser Tyr His Leu Thr Val Pro His Thr Pro Gln
35 40 45

Leu Asn Gly Val Ser Glu Arg Met Ile Arg Thr Ile Thr Glu Lys
50 55 60

<210> 51
<211> 63
<212> PRT

<213> Unknown

<220>

<223> Integrase sequence of Tnt1 retrotransposon

<400> 51

His Lys Arg Met Gly His Cys Asp Tyr Cys Lys Leu Lys Arg Leu Arg
1 5 10 15

Ser Asp Asn Gly Gly Glu Tyr Thr Ser Arg Glu Phe Glu Glu Tyr Cys
20 25 30

Ser Ser His Gly Ile Arg His Glu Lys Thr Val Pro Gly Thr Pro Gln
35 40 45

His Asn Gly Val Ala Glu Arg Met Asn Arg Thr Ile Val Glu Lys
50 55 60

<210> 52

<211> 62

<212> PRT

<213> Unknown

<220>

<223> Integrase sequence of Ty1 retrotransposon

<400> 52

His Arg Met Leu Ala His Cys Pro Asp Cys Ser Val Leu Val Ile Gln
1 5 10 15

Met Asp Arg Gly Ser Glu Tyr Thr Asn Arg Thr Leu His Lys Phe Leu
20 25 30

Glu Lys Asn Gly Ile Thr Pro Cys Tyr Thr Thr Thr Ala Asp Ser Arg
35 40 45

Ala His Gly Val Ala Glu Arg Leu Asn Arg Thr Leu Leu Asp
50 55 60

<210> 53

<211> 59

<212> PRT

<213> Unknown

<220>

<223> Integrase sequence of Ty4 retrotransposon

<400> 53

His Lys Arg Met Gly His Lys Val Arg Glu Ile Asn Ser Asp Arg Gly
1 5 10 15

Thr Glu Phe Thr Asn Asp Gln Ile Glu Glu Tyr Phe Ile Ser Lys Gly
20 25 30

Ile His His Ile Leu Thr Ser Thr Gln Asp His Ala Ala Asn Gly Arg
35 40 45

Ala Glu Arg Tyr Ile Arg Thr Ile Ile Thr Asp
50 55

<210> 54
<211> 60
<212> PRT
<213> Candida albicans

<400> 54

His Leu Met Ser Asn His Cys Lys Val Cys Lys Val Ala Tyr Phe Arg
1 5 10 15

Ser Asp Asn Ala Pro Glu Phe Pro Gln Pro Ser Asp Leu Ala Glu Phe
20 25 30

Gly Ile Trp Arg Glu Thr Ile Ala Ala Tyr Ser Pro Glu Leu Asn Gly
35 40 45

Leu Ala Glu Val Val Asn Lys Leu Ile Leu Gln Gln
50 55 60

<210> 55
<211> 63
<212> PRT
<213> Unknown

<220>

<223> Reverse Transcriptase sequence of 1731 retrotransposon

<400> 55

His His Met Asp Val Cys Thr Ala Tyr Leu Asn Ser Glu Leu Lys Asp
1 5 10 15

Thr Val Tyr Met Lys Gln Pro Gln Gly Phe Thr Asp Ala Ala Asn Pro
20 25 30

Asp Gln Val Leu Leu Leu Arg Lys Ala Ile Tyr Gly Leu Lys Gln Ser
35 40 45

Gly Arg Glu Trp Asn Ile Leu Val Tyr Val Asp Asp Leu Ile Leu
50 55 60

<210> 56
<211> 61
<212> PRT
<213> Unknown

<220>

<223> Reverse Transcriptase sequence of copia retrotransposon

<400> 56

His Gln Met Asp Val Lys Thr Ala Phe Leu Asn Gly Thr Leu Lys Glu
1 5 10 15

Glu Ile Tyr Met Arg Leu Pro Gln Gly Ile Ser Cys Asn Ser Asp Asn
20 25 30

Val Cys Lys Leu Asn Lys Ala Ile Tyr Gly Leu Lys Gln Ala Ala Arg
35 40 45

Cys Trp Phe Val Leu Leu Tyr Val Asp Asp Val Val Ile
50 55 60

<210> 57
<211> 63
<212> PRT
<213> Unknown

<220>

<223> Reverse Transcriptase sequence of Tnt1 retrotransposon

<400> 57

Glu Gln Leu Asp Val Lys Thr Ala Phe Leu His Gly Asp Leu Glu Glu
1 5 10 15

Glu Ile Tyr Met Glu Gln Pro Glu Gly Phe Glu Val Ala Gly Lys Lys
20 25 30

His Met Val Cys Lys Leu Asn Lys Ser Leu Tyr Gly Leu Lys Gln Ala
35 40 45

Pro Arg Gln Trp Tyr Leu Leu Leu Tyr Val Asp Asp Met Leu Ile
50 55 60

<210> 58
<211> 60
<212> PRT
<213> Unknown

<220>

<223> Reverse Transcriptase sequence of Ty1 retrotransposon

<400> 58

Thr Gln Leu Asp Ile Ser Ser Ala Tyr Leu Tyr Ala Asp Ile Lys Glu
1 5 10 15

Glu Leu Tyr Ile Arg Pro Pro Pro His Leu Gly Met Asn Asp Lys Leu
20 25 30

Ile Arg Leu Lys Lys Ser Leu Tyr Gly Leu Lys Gln Ser Gly Ala Asn
35 40 45

Trp Tyr Ile Cys Leu Phe Val Asp Asp Met Val Leu
50 55 60

<210> 59

<211> 47
<212> PRT
<213> Unknown

<220>

<223> Reverse Transcriptase sequence of Ty4 retrotransposon

<400> 59

Lys Thr Leu Asp Ile Asn His Ala Phe Leu Tyr Ala Lys Leu Glu Glu
1 5 10 15

Glu Ile Tyr Ile Pro His Pro His Asp Arg Arg Cys Val Val Lys Leu
20 25 30

Asn Lys Ala Leu Tyr Gly Leu Lys Gln Ser Pro Lys Glu Trp Asn
35 40 45

<210> 60
<211> 63
<212> PRT
<213> Candida albicans

<400> 60

Gln His Leu Asp Val Glu Ser Ala Tyr Leu Asn Ala Ser Ile Thr His
1 5 10 15

Ser Asn Pro Ile Tyr Val Phe Pro Pro Lys Ser Val Pro Leu Lys Lys
20 25 30

Asn His Cys Trp Leu Leu Lys Arg Ser Val Tyr Gly Leu Lys Gln Ser
35 40 45

Gly Leu Glu Trp Tyr Leu Gly Leu Tyr Val Asp Asp Ile Leu Met
50 55 60

<210> 61
<211> 24
<212> PRT
<213> Unknown

<220>

<223> RNase H sequence of 1731 retrotransposon

<400> 61

Ala Phe Thr Gly Phe Val Asp Ala Asp Trp Gly Gly Asp Arg Leu Asp
1 5 10 15

Arg Lys Ser Tyr Thr Gly Tyr Val
20

<210> 62
<211> 24
<212> PRT
<213> Unknown

<220>

<223> RNase H sequence of copia retrotransposon

<400> 62

Lys Ile Ile Gly Tyr Val Asp Ser Asp Trp Ala Gly Ser Glu Ile Asp
1 5 10 15

Arg Lys Ser Thr Thr Gly Tyr Leu
20

<210> 63

<211> 24

<212> PRT

<213> Unknown

<220>

<223> RNase H sequence of Tnt1 retrotransposon

<400> 63

Ile Leu Lys Gly Tyr Thr Asp Ala Asp Met Ala Gly Asp Ile Asp Asn
1 5 10 15

Arg Lys Ser Ser Thr Gly Tyr Leu
20

<210> 64

<211> 23

<212> PRT

<213> Unknown

<220>

<223> RNase H sequence of Ty1 retrotransposon

<400> 64

Lys Leu Val Ala Ile Ser Asp Ala Ser Tyr Gly Asn Gln Pro Tyr Tyr
1 5 10 15

Lys Ser Gln Ile Gly Asn Ile
20

<210> 65

<211> 23

<212> PRT

<213> Unknown

<220>

<223> RNase H sequence of Ty4 retrotransposon

<400> 65

Lys Val Ile Ala Ile Thr Asp Ala Ser Val Gly Ser Glu Tyr Asp Ala
1 5 10 15

Gln Ser Arg Ile Gly Val Ile
20

<210> 66
<211> 23
<212> PRT
<213> Candida albicans

<400> 66

Val Ile Glu Cys Phe Ser Asp Ala Ser Phe Ala Pro Gly Leu Asp Arg
1 5 10 15

Lys Ser Ile Ser Gly Thr Leu
20

<210> 67
<211> 67
<212> RNA
<213> Candida albicans

<400> 67

uagggagguc agggucagga gccccccccc ugaaccagg auaaccuca aagucggggg 60
gcaaccc 67

<210> 68
<211> 90
<212> RNA
<213> Candida albicans

<400> 68

ugaaaaacag gugcugcuuc uauuaauugu guaaugaaua uacauaaug cagcaaaacc 60
acguuuccag uagaaauucu cauucucuua 90

<210> 69
<211> 392
<212> DNA
<213> Candida albicans

<220>
<221> misc_feature
<222> (1)..(392)
<223> sequence of clone SGY-1

<220>
<221> variation
<222> (30)..(30)
<223> 'a' replaced by 'g' in SC5-2

<220>
<221> variation

<222> (172)..(172)
<223> nucleotide 'a' is replaced by 'g' in SC5-1, SC5-2, SA4-1, SA4-2, 759-1, 759-2 and p36 or by 't' in ATC-1 and ATC-2

<220>
<221> variation
<222> (173)..(173)
<223> nucleotide 'g' is replaced by 'a' in ATC-1,ATC-2, SA4-1 and SA4-

<220>
<221> variation
<222> (235)..(235)
<223> nucleotide 'a' is replaced by 'g' in SC5-1, SC5-2, SA4-1 and SA4

<220>
<221> variation
<222> (292)..(292)
<223> nucleotide 'g' is replaced by 'a' in SC5-1, SC5-2, 759-1, 759-2 and p3

<220>
<221> variation
<222> (294)..(294)
<223> nucleotide 't' is replaced by 'a' in SC5-1, SC5-2, 759-1, 759-2 and p3

<220>
<221> variation
<222> (297)..(297)
<223> nucleotide 't' is replaced by 'c' in SC5-1, SC5-2, 759-1 and 759

<220>
<221> variation
<222> (303)..(303)
<223> nucleotide 't' is replaced by 'c' in 759-2

<220>
<221> variation
<222> (311)..(311)
<223> nucleotide 't' is replaced by 'c' in 759-2

<220>
<221> variation
<222> (350)..(350)
<223> nucleotide 't' is replaced by 'c' in SA4-2

<220>
 <221> variation
 <222> (371)..(371)
 <223> nucleotide 'g' is replaced by 'a' in 759-1, 759-2 and p36

<400> 69
 tggttggttg tgcactatgt tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
 gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
 ataaataagg gtaggaaata ccaacatccc agaatatcaa cgagatagaa gagaggagtt 180
 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
 acacgtctaa tctcaggtaa agaaagttta tattccatca gattagaagt cgatagtgat 300
 aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
 gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 70
 <211> 392
 <212> DNA
 <213> Candida albicans

<220>
 <221> misc_feature
 <222> (1)..(392)
 <223> sequence of clone SGY-2

<400> 70
 tggttggttg tgcactatgt tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
 gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
 ataaataagg gtaggaaata ccaacatccc agaatatcaa cgagatagaa gagaggagtt 180
 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
 acacgtctaa tctcaggtaa agaaagttta tattccatca gattagaagt cgatagtgat 300
 aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
 gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 71
 <211> 392
 <212> DNA
 <213> Candida albicans

<220>
 <221> misc_feature

<222> (1)..(392)
<223> sequence of clone SC5-1

<400> 71
tggttggttg tgcactat ttt tgtgtcagag actgatcaat gaaaatgatg gttattatga 60
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt 180
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctaggcgtgt 240
acacgctcaa tctcaggtaa agaaagt tta tattccatca gattagaagt caaaagcgat 300
aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 72
<211> 392
<212> DNA
<213> Candida albicans

<400> 72
tggttggttg tgcactat ttt tgtgtcagag actgatcaat gaaaatgatg gttattatga 60
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt 180
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctaggcgtgt 240
acacgctcaa tctcaggtaa agaaagt tta tattccatca gattagaagt caaaagcgat 300
aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 73
<211> 392
<212> DNA
<213> Candida albicans

<400> 73
tggttggttg tgcactat ttt tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
ataaataagg gtatgaaata ccaacatccc agaatatcaa cgtaatagaa gagaggagtt 180
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
acacgctcaa tctcaggtaa agaaagt tta tattccatca gattagaagt cgatagtgat 300

aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 74
<211> 392
<212> DNA
<213> Candida albicans

<400> 74
tggttggttg tgcactat tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
ataaataagg gtatgaaata ccaacatccc agaatatcaa cgtaatagaa gagaggagtt 180
tcaatatata tcttgatgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
acacgtcaa tctcaggtaa agaaagttaa tattccatca gattagaagt cgatagtgat 300
aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 75
<211> 392
<212> DNA
<213> Candida albicans

<400> 75
tggttggttg tgcactat tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
ataaataagg gtatgaaata ccaacatccc agaatatcaa cggaatagaa gagaggagtt 180
tcaatatata tcttgatgaat aataacttcg ttctaattca ctatacacia ctaggcgtgt 240
acacgtcaa tctcaggtaa agaaagttaa tattccatca gattagaagt cgatagtgat 300
aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 76
<211> 392
<212> DNA
<213> Candida albicans

<400> 76
tggttggttg tgcactat tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120

ataaataagg gtatgaaata ccaacatccc agaatatcaa cggaatagaa gagaggagtt 180
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctaggcgtgt 240
acacgctcaa tctcaggtaa agaaagttta tattccatca gattagaagt cgatagtgat 300
aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgc attattgatt 360
gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 77
<211> 392
<212> DNA
<213> Candida albicans

<400> 77
tggttggttg tgcactatct tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gagaggagtt 180
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
acacgctcaa tctcaggtaa agaaagttta tattccatca gattagaagt cgatagtgat 300
aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 78
<211> 392
<212> DNA
<213> Candida albicans

<400> 78
tggttggttg tgcactatct tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gagaggagtt 180
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
acacgctcaa tctcaggtaa agaaagttta tattccatca gattagaagt cgatagtgat 300
aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 79
<211> 392
<212> DNA
<213> Candida albicans

<400> 79
 tgttggtttg tgcactatatt tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
 gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
 ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt 180
 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
 acacgctcaa tctcaggtaa agaaagttta tattccatca gattagaagt caaaagcgat 300
 aatcatttcg tcccaaatta gcgttgata aattcagtcc tcagatttgt attattgatt 360
 gatagtttcg aagtttgaag gtacagaatt tc 392

<210> 80
 <211> 392
 <212> DNA
 <213> Candida albicans

<400> 80
 tgttggtttg tgcactatatt tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
 gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
 ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt 180
 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
 acacgctcaa tctcaggtaa agaaagttta tattccatca gattagaagt caaaagcgat 300
 aatcatttcg tcccaaatta gcgttgata aattcagtcc tcagatttgt attattgatt 360
 gacagtttcg cagtttgaag gtacagaatt tc 392

<210> 81
 <211> 392
 <212> DNA
 <213> Candida albicans

<400> 81
 tgttggtttg tgcactatatt tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
 gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
 ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gagaggagtt 180
 tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
 acacgctcaa tctcaggtaa agaaagttta tattccatca gattagaagt caaaagtgt 300
 aatcatttcg tcccaaatta gcgttgata aattcagtcc tcagatttgt attattgatt 360
 gatagtttcg gagtttgaag gtacagaatt tc 392

<210> 82
<211> 392
<212> DNA
<213> Candida albicans

<400> 82
tgttggttg tgcactattt tgtgtcagaa actgatcaat gaaaatgatg gttattatga 60
gaatggaaaa tttttccatc acacatcagg tgatgacaga actaaactat attgtgtagt 120
ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt 180
tcaatatata tcttgtgaat aataacttcg ttctaattca ctatacacia ctagacgtgt 240
acacgtcaa tctcaggtaa agaaagttta tattccatca gattagaagt cgatagtgat 300
aatcatttcg tcccaaatta gcgttgata aattcagtc tcagatttgt attattgatt 360
gatagtttcg aagtttgaag gtacagaatt tc 392

<210> 83
<211> 137
<212> RNA
<213> Candida albicans

<400> 83
uauuccauca gauuagaagu caaaagcgau aaccuuuucg ccccaaauua gcuuguaua 60
aaucagucc ucagauuugu auuauugauu gauaguucga aguuugaagg uacagaauuu 120
cacaauga guuccgc 137

<210> 84
<211> 39
<212> RNA
<213> Candida albicans

<400> 84
gccugcgugg cgaaaugguu aucgcuuuug acuuuauc 39

<210> 85
<211> 455
<212> DNA
<213> Candida albicans

<220>
<221> misc_feature
<222> (1)..(455)
<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 85

tggtttgtgc ctatattgtg tcagaaactg atcaatgaaa atgatgggta ttatgagaat	60
ggaaaatttt tccatcacac atcagggtgat gacagaacta aactatattg tgtagtataa	120
ataaggggtat gaaataccaa catcccagaa tatcaacgag atagaagaga ggagtttcaa	180
tatatatctt gtgaataata acttcgttct aattcactat acacaactag acgtgtacac	240
gtcfaatctc aggtaaagaa agtttatatt ccatcaataa tataaagcca tgatgtcttg	300
ttaatcaatt gatgtgtaca aatgggttatg ttgaaattga aaatagtttc gaaataatcg	360
ttgtgctact gggtgaggca tgagtttctg ctctctcact ataggtctta gtgttgactg	420
tcatatcttt tgtctagaat annnnnnnnn nnnnn	455

<210> 86
 <211> 20
 <212> DNA
 <213> Candida albicans

<400> 86 tatatatggt aatatacact	20
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<210> 87
 <211> 20
 <212> DNA
 <213> Candida albicans

<400> 87 gagtctgtaa gaaatcacca	20
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<210> 88
 <211> 20
 <212> DNA
 <213> Candida albicans

<400> 88 gccactttgg agtacattcg	20
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<210> 89
 <211> 20
 <212> DNA
 <213> Candida albicans

<400> 89 tattcggttt taaataaatt	20
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<210> 90
 <211> 20
 <212> DNA
 <213> Candida albicans

<400> 90
aaaaaataga gaacgcgctg

20

<210> 91
<211> 20
<212> DNA
<213> Candida albicans

<400> 91
tctttctttt tcttgacact

20

<210> 92
<211> 20
<212> DNA
<213> Candida albicans

<400> 92
ttctattttt ggttttcttg

20

<210> 93
<211> 20
<212> DNA
<213> Candida albicans

<400> 93
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<210> 94
<211> 20
<212> DNA
<213> Candida albicans

<400> 94
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<210> 95
<211> 20
<212> DNA
<213> Candida albicans

<400> 95
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<210> 96
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<213> Candida albicans

<400> 96
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<213> Candida albicans

<400> 98
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<212> DNA
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<400> 99
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<210> 100
<211> 994
<212> DNA
<213> Unknown

<220>
<223> sequence of retrotransposon from unknown organism

<400> 100
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gatttaatcc aaatcaatac cttttgtttt gtagaaatct ttgcttctt caatttgtat 180
tttcaattct ttgtatttat gttctttgtc ttggaatgta acaattcccc aacctaacgt 240
tgataaggca taagacccaa atgtgactaa tccccacat ggcaagtatg gcaatatttc 300
atcgtgtatt ttagctggag ttggaatcac acctgtgata agagcaaaat aaatagctga 360
taaggcaaaa attgttaatc ctgtttcagt agcttttagtc attcttatag ttagacttgt 420
taaagggtag ttgtgttaat tgaagatatg ctggaaaact atacttttcg ttgttttttt 480
ttttcaatct aggtcgggtg tgctgttatt ttttttctct cttcttggtt cttagtattg 540
gattatatgt tggtttatgc gacgtttgtg tcagggaat aacaccttga tataagtcgt 600

gcgtattagg tcaacattgg tgaaaaattt gcactcatcg agagccagga attagtataa 660
aaagaagaga aaagaaagat atttaggata tttattatat agggaccgag tttcaggaga 720
cacttttagt gggcgtaaac ttcattcact ctgttttttg cttattacaa attatcacct 780
atogtgtact aggactaatt ctcacgaata ttccgtgtat acaaacactt attgccaaact 840
tatggtgcgg aactttatth gtctgaacca aaatcaaagt cacatcattt aaatgaacgt 900
tgacataaat agattcttta ttcaatagaa acaatttctt cctttttctt ttctttgtat 960
tattggttag atttccattc catatacaca caag 994

<210> 101
<211> 1348
<212> DNA
<213> Unknown

<220>
<223> sequence of retrotransposon from unknown organism

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gctcaatgat ttatttttagg tttatatgtg gatgatattt taatggacag aatctcagat 180
ggaatcgta tcagatttgt tgaacaagag agagtttatt tcgcgtcaaa atcaatttag 240
gtctcatgac agaatatgtg agataaaatg tccacgtaag caaaactggg tgatactttg 300
aattaagaga tactcctaaa taagcaaacc aaggatttta aactacacaa ttcgtatggt 360
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cgaatattcc gtgtatacaa acattatacg tgtctgtaac tacgcgaaac tacttcgtct	1080
cagttttttg ttacaaacaa ctttccgtat agacctgaga ttttgtcagc ttgattgaat	1140
ggaagagttt actaaagtac cagaaagggtg ttttatagat aacatgtaga tatataaaaa	1200
tgttatatta caaatgactt ccaaaagaaa ctgtacgaat tttgctgttt attaaaaacc	1260
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acaagttcta ctttcccgac aatgctaa	1348

<210> 102
 <211> 3034
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 102

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aagtcgtgag tattaggtca acattggtga aaaatttgca ctcatcgaga gccaggaatt	180
agtataaaaa gaagagaaaa gaaagatatt taggatattt attatataga gaccgagttt	240
caatagacac ttttagtggg cgtaaaactt atttactctg ttttttgctt attacaaatt	300
atcacctata gtgtactagg actaattctc acgaatatc cgtgtataca aacaaaattt	360
tcgaaactag tcaatcacia caaatgtgtt tgagttcaac tgaaacgata acaaccatca	420
taattcgatt gaatactttg tgcgtctctt ttctttctat gcattctact acttgctgac	480
tacatatata cagccatgac ttgcatatat cctagcaact cctccctccc ccctattggt	540
gttggttttt ttaataatat ttagtatatg tatcaatggt aaaaactatt ttttgattt	600
ttttttggtt tgtaaatttt gatagttttt ttattgaaaa cttcaaactt caaaaatttc	660
taataacaac aacgacaaca attattaaat gatactctac tcaaaaagaa aatttgatga	720
aatgccaaga acaatataat ttagtcagta cattaatact caattacaac aacaacaaca	780
acaacaacaa caacaactgt tcaatgcaat aataagagag aaaccaatag aactaattta	840
gtttttcaaa tagccaacct tcaaaaaaaaa ataaattatg tgaatgcata aaatatgtat	900
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gccaaaaaaa aaaaaatatg caaccttttt ccttcctcca cctccttctt atttcgtgaa	2940
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atcaattgat ggcaaatatg taagtaagtt cgat	3034

<210> 103
 <211> 3504
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

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aaaataaaat tactcaattt gtaaataagca aatccaggaa ttatcaagta cccataccat	180
actttattac ttccaaaaat aatcatcaaa atategaacc cccaagtcaa atagataaca	240
tcaaaataat attcatataa actccccagt aatctaattgt cttcaccact tgaaactaaa	300
gagttaccat tggatatattt gggacgacca aatttttcca aagaatattg taaaaatata	360
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attaaaaaca caataatggt aattgatgag gaaatgatta ataattgatt taatatgttg	480
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tcacctgagg aggttagtca atttgagatt gtgcgaggga aaaaaaacga cctccatata	660
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cacgacaatc ctgagacgga agtcgatcgt cgatgcccatt ggtgcgtggg gaaaaatttt	780
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ggagtacaac actttacatt tottccgaaa caataactat ataaacccat gtaagtctcc	3420
cctcttttgt ttcaaacgtc ttatcaattt ttctcttcac tactttttcca acttaacaat	3480
cttcacttat aatctcaacg aatc	3504

<210> 104
 <211> 3955
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 104

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actttttttt ttagtcaaac tctacgaaat gaaattcaaa gagaataatc cacagaagag	180
gagagagggc aaaagtgggg ggaccaaagg gggttagaaa acaggaaaca gcaatagaga	240
gcaataattg aaaaatagtg ttgtcaacaa tagaacaat tggtaaaact ttaaatgcaa	300
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gcaaagagaa taccgagtta atagtgagtc tattagtgtt gcaggaaaag ttatacgaac	660

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<212> DNA
<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 105

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ctagccaaaa atttgtgtac tgcaattggt cgctatagag agatataccta gccggaatgc	120
acgacaatcc tgagacggaa gtcgatcgtc gatgcccatg gtgcgtggtg aaaaattttc	180
ttagaaaatt tgttctttcc ttcaactgct tttaagagaa gggaggttca agtggtttaa	240
gtacgacggt cacaaagatt gcggcttatg aggcccgaaac tgagttgaaa taaaaatca	300
agatataatt atatacctta cttgtctata ttgttttata atacattctt cagatattta	360
aatttctgtg tatcatccta taaaacagag atacattcag tacatttagt atactgagtg	420
aactggtacc tgtgacattc aagataactg tttcgcgcac gctggcagac gaacagcaat	480
tctgtaattg tcgtagagta gcaacaaatc ttcccgatga ttggtacttg tgttagtcta	540
cacgacatgt gttttggtac acttgaactg tatgtccaag aatggaaaca tatgcgggaa	600
ggacgcgaaa gatgagtttg gtatagaagg gataagaact gtaaaatata ttatgtagtt	660
atatatttta attatgggaa attgagtgtt tattctgttc aacaagtttc aaccgtagag	720
attacattta aagtctgtgg tcgaaatcca caagatacag caaattcatg aattcaccta	780
tttaaataca gtttaccag caccattgcc tagaacttgc catatcatca attaagtcag	840
acattactaa tttgagcaaa gcttttagct taatgggcca actaatttaa gtcgaattgg	900
taatgcaatc tgttcttcat ttgagtcgct tgctacggct ccatgacaca tccatttgat	960
tgttttaatt cgagcaatta tccaccataa ctctcagtaa tatcattaac agttttacgc	1020
ttaataagca tagaaagttg tatgaagttg tctcctaggt atgctagaga gatttgtata	1080
tacgaccagt aaagagtgtg atgaggtgtt tactgtaggg taaattgcaa ttgacttgag	1140
ttgatagcgg ttattacaaa agtatagatt caacaaatta agacaagtac caaacgatag	1200
gccgaatgtg acttataccg ttgaagttca agcgttttta acaaatagaa atgtgagatt	1260
aatgagttcg acaaagtgtt tactagatac tattaatttc gatgtactat ataagtttaa	1320
ccagctataa ccggcagagc agacttcctg aaactcaaat tggttgtgtt tggacttgag	1380
ttacaccaca aagtttgaca atcgtgagga catagcaacc tatcaagcca ctca	1434

<210> 106

<211> 1608
<212> DNA
<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 106

tgctagtatg tattttggct ctttgatcct gaatgcgaca atgcaataca aatagtagaa	60
ataatgatgg tgatactact agtattaata ataatccgag aaacgatatc acaaaataaa	120
tcagtgccca atgaggttga tgcacaaata ttagtgggtg gtaaaactaa agagaatatc	180
tcgctatgat ttctattgat aagaaaagat gagagattaa ggaaatatct tctgtaaagt	240
tgtatcgcca cctttttttt ttgtagtagt agtatcggtt ttggttttgg ttttctcatt	300
agttaagatt cttgcgataa ggcacgacct tgatcatttg catgtttctc gtttaattgt	360
ttttatttct ttttttttta tgggtgtgtg tagtagttac agatatcgac ggttgcaagt	420
gcacgagtgc tgcgactgac cggatcgtca tgctaaaaga ttcaggggtg tgtaagagcg	480
tgccaagtgc aggaggaacc aacatttcac aactgcttca ggatagggca ttctttttct	540
tctttctatt tgatctagcc ttgcgtctat tcgtgttggt ggttggtaca agcgaatatc	600
ccaataaggt ttttgttgcc tatgtgcac gtgttgtagc atagtaacga gagatacgat	660
tcttcttctt ctcttctccc ttttctttgg attgctttat atttatatat atatattgtc	720
atcatcgtca cgaaattcac tatcattatc aattattttg ttttttctct atctttgtcc	780
tcctcgttta atccttatca cagttttggg ttggtgcaat ttcttttcat tctccagttg	840
aggcttacac tttctcttgg agtttccggt tataattttt acacacacaa aagcacaaac	900
tacactttgt cttcacagtg tataacagat accacagtat tactaagggg gaaaactaac	960
ctaaccaaag ggactgacaa aataagtga aagactacaa atgacgccct taatatacga	1020
gagagaattg aaaagacata cacataatgt tcgctataga gagatttcct agccggaatg	1080
cacgacaatc ctgagacgga agtcgatcgt cgatgcccat ggtgcgtggt gaaaaatttt	1140
cttagaaaat ttgttctttc cttcaactgc ttttaagaaa gggaggttca agtggtttaa	1200
gtacgacggt cacaaagatt gcggcttatg aggcccgaac tgagttgaaa taaaaatca	1260
agatataatt atatacctta cttgtccata ttgttttata atacattctt cagatattta	1320
aattttctgt tatcaacct aaaaacagag atacattcag tgcatttagt atactgagt	1380
aactggtacc tgtgacattc aagataactg tttcgcgcac gctggcagac gaacaattgc	1440
ggcgaaaaaa aaaagaggtc gccaaaacta aactgttggg acgatttgct gccaatcaca	1500

atgaaaaaaaa aaaagaacag ttggtttgaa acttcttctcct ctaatacaga attaaactgat 1560
 ctttctatca ctgttttaaac tattcattac tctcaagaac ttaccatg 1608

<210> 107
 <211> 1385
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 107

aataagtgga tttatcatta ctattatcgt aatgctcaat caggggagtg ttggtttgtg 60
 cactattttg tgtcagaaac tgatcaatga aaatgatggg tattatgaga atggaaaatt 120
 tttccatcac acatcaggtg atgacagaac taaactatat tgtgtagtat aaataagggt 180
 atgaaatacc aacatcccag aatatcaacg agatagaagg gaggagtttc aatatatatac 240
 ttgtgaataa taacttcggt ctaattcact atacacaact agacgtgtac acgctcaatc 300
 tcaggtaaag aaagtttata ttccatcaac agtactagta ttagtattag tagttgcttt 360
 gtcatatata aatagattaa ttaaactaac taacaaccta tatcaaatac aatcatcagt 420
 tatatcatca tcaacatatt catcatcttt attcattcta taaattgtca ttgccatact 480
 tgcaaaatc aataaactca taatccaatc cggcaaagca attccatata attcaatgag 540
 attaaatggt aaatctaaga aattcccaat taattcaata ataagcatca ttttatcaaa 600
 tcgtaaatct ttttaacttt ttttgtattt tttatttaaa tcttcattta taaaatttat 660
 tccagtcttg ttttagtggt tggtagtaga atttaataaa tcaacttcaa tattaacttt 720
 tctaatttta cgtattacat ttagtaattg agatatgggt ttcttgatta aaaaaaccaa 780
 tattaatacc caaattttat tgggttggtt taaaaatcga tttaaaaatt gtgggaacat 840
 tggtaaattt gataataaat gtaaattatc taataaattg gcaagatttt ctaaaatatt 900
 aacaaacata aattctattt ttttcaaact aaatgtattt ggtctatagt attttatagg 960
 tttattatta ttattaggtt tactccctga cttgggtttc ttactggag attgacctcg 1020
 ttcttgtcga ttgttgtgag atgatttatt aatatcaaatt ttattaaata ctgaagggtg 1080
 ttttggtttt ggaggtaatt tagccttagt aggggttgat aatggttggt atcgactttg 1140
 taacttttgt tgttgttgtt gttgtgctag taaaatggtt aatttatcaa gtttatctga 1200
 tgtgattgaa gtattaccct gttgttggtc tttttgagct agaagaagta aattattgat 1260

aatttattgt tgacgtgagt caggattagg atcaattgaa gtatgtttta agtttaattt	1320
ttgaattaaa tcaatattct cctgtattgt tgtagtgaac attacggata ttaataataa	1380
ataaa	1385

<210> 108
 <211> 1483
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 108	
tgaataatca ggggatgcaa gttattgatt ttgccagtat ccaattttac ttgtggtttc	60
gagaaagtgc tttctctcat tggtagttta aggttaactg aaattcaaatt tataggagtt	120
tttgaacata aaaagcatat acaacttgag tagcatgtat atattgcata taaagattct	180
ttttttttgt aattgagttt gccaaacatt ttagtcactc ccaatatatc gtcaactcgt	240
aaatgtgata attcaggtca agtgcctacc tctaacgatt agccaacatt ttttgaaaca	300
aaaatatatt tcaaaggaac acagtgaaaa cctctctatg taggctgaca ggtgaaaatt	360
atgaattaat tgcattggcc aatgacaaat gaatagacaa aacagcaaatt aagggtgcaa	420
aagtagccca aacaaactag atttcgggta cgaattttcc atctttcaaa acaatgaatt	480
tgtttagagc tctgtgccat ttattgcaac taaaatgaat atgcaattaa acaatcagag	540
atgtattgga ttatccccgt ggtatacttt tgagttcacc atttgttttt tttttggggt	600
taaattagtg ctctactaa aaatcgcatt tatcttacac tcaccatttt gataagttat	660
ctctgggtcaa tcgcaaatac tatgcttcta attaagagtt ctatgtaaatt cccattttatt	720
ttgatcaatc tattggtttg aagtaagagt tgattttctg taaagattta tttgacagtg	780
tagttcggtg tcaaaaatat attatgatgt aactaaaaa aactaaatt tcaagtcaat	840
ggggaacaca aaactgaatt aattactata tgttggtttg tgcactatct tgtgtcagaa	900
actgatcaat gaaaatgatg gttattatga gaatggaaaa tttttccatc acacatcagg	960
tgatgacaga actaaactat attgtgtagt ataaataagg gtatgaaata ccaacatccc	1020
agaatatcaa cgagatagaa gagaggagtt tcaatatata tcttgtgaat aataacttcg	1080
ttctaattca ctatacaca ctagacgtgt acacgctcaa tctcaggtaa agaaagttta	1140
tattccatca ctatataaca acaatcaggc tttgcaaaaa aacattttaa actaatactg	1200
gtaatatgga aatataacgc ctctagttc tacgcacgtg gcacccctta tctattttatt	1260

caatttacc	ctaatttatg	aattagctta	ataagagcag	tcaaattaac	acggctcaat	1320
taatagtact	taataatatg	aagccgatca	attaaccgat	cctttgaata	atttgaaaat	1380
aaaataaagt	aatataaata	ggtatgcatt	ttccctacat	ttatttctct	tttctatttt	1440
aatttgtttc	ctaaacagca	acaacaacaa	ttgaaattca	aaa		1483

<210> 109
 <211> 879
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 109	
ggctcgtaga	60
ttcgggtatac	
ttgtctagaa	
taaaaatgaa	
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agttgaaatg	
tcaggtggtg	120
gtggtggttt	
tttttttagat	
ttcaaaaact	
atacatactc	
ctatgagatc	
aattttcttg	180
attgaatatac	
ttggtaaaat	
ggttatgagt	
tcattttctg	
ccaaaaaggt	
aattttctgat	240
ggcataagat	
tcccttgaag	
gttttttggg	
agtaccatga	
cgggttaagg	
attatttgtt	300
aatgggttaa	
actagatagt	
agtagtctat	
atttaattta	
tttttttttt	
tttgacacct	360
tgtgcgaaag	
atctctgttg	
gtttgtacac	
tattttgtgt	
cagaaactga	
tcaatgaaaa	420
tgatggttat	
tatgagaatg	
gaaaattttt	
ccatcacaca	
tcaggtgatg	
acagaactaa	480
actatattgt	
gtagtataaa	
taagggtagt	
aaataccaac	
atcccagaat	
atcaactata	540
tagaaggag	
gagtttcaat	
atatatcttg	
tgaataataa	
cttcgttcta	
attcactata	600
cacaactaga	
cgtgtacacg	
ctcaatctca	
ggtaaagaaa	
gtttatattc	
catcaatctc	660
tctcgatggt	
gtaaagagac	
gcgtcaatta	
acaataaaact	
ctaattttgt	
ttttcttcta	720
caaaactacc	
aaacataatc	
atgtcaaggt	
aaattacaat	
gatatttaat	
tacgtaaata	780
cttctatacc	
cttattgata	
ttcaatcatt	
ttcttcttat	
acgtggaagt	
tcttccagat	840
gtcatggcct	
tggcccttct	
agcaggtttt	
ggaccgtcac	
tatctctact	
atacgggtca	879
aatccacgtc	
tctgtctacc	
attagtcta	

<210> 110
 <211> 974
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 110
 acccgtctag tatcagctcg tcgttttcaa gtatgttggt catgtccagg ttgttgctcg 60
 tgggtggcagg tactttgtcg tccaatttta ggtcctcgta gtccatgttg gacaacatgt 120
 cttegtcggt attgccgttg atgtcaaagc caataaagtc gtcaaagttg tcaaactttt 180
 gtggggcggt ctctgctttc tttctggcct ctgctttctg tttgttttac acttttcgtc 240
 tttaattata gtttcgaaga atttcctagg aacttaagaa tttgtaggag aatgctaata 300
 agaagttgta tttcttaatt gaaagttata attgtaagaa tatattgtat aaaagatgag 360
 ttgataaaga aaagatataa aaagtcctat aaaaaagtat tgtaaaataa aagtatataa 420
 aatcaagta aaatagaata tttgcacaca aattaaaagt agtgcaaatt tgacagaaaa 480
 gttgttggtt tgtgcactat tttgtgtcag aaactgatct atgaaaatga tggttattat 540
 gagaatgaaa aatttttctt tcacacatca ggtgatgaca gaactaaact atattgtgta 600
 gtataaataa gggatgaaat accaacatcc cagaatatca actatataga aggcaggagt 660
 ttcaatatat atcttgtaga taataacttc gttctaattc actatacaca actaggcgtg 720
 tacacgtca atctcaggta aagaaagttt atattccatc aaaagtaaaa taaaacactt 780
 cttegtctcc tctgctttct tggttgctc tgccttcttg gcctcttctt ccttctttct 840
 tgccgttct tctttgactt tcaattcgtc aagtttcttt ttcttttcaa ccataacgcc 900
 gagacaccac tctgcatcat tgagtttcga cactgtttgg tctagaatag catggaagtt 960
 ttggatttcg ccgt 974

<210> 111
 <211> 3868
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<220>
 <221> misc_feature
 <222> (1)..(3868)
 <223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 111
 aatgaagtaa cttttttcaa ggcaacatct attcttttat taatctcgac gtctgtttga 60
 ttaagttgct ctaacatttt atttagatcc ttctctatat tttctgcaat atcaaacacc 120
 gattgctttt tgtctgaagt tgctgggtata tcaccacttc cgccaattgt cgtatttcca 180

ctgtcctttg ttactgacag attggcactg acattacctg aattgttcat gtttgctggt	240
gaaagagcag gaactgtact tggataagca gccgattcaa aagaagatgt ggacatgagt	300
gtcaagaaaa tgtgtagaat cagtacaaga ctggaaaaca gaaggaacaa agtgaactgg	360
atattgtagt tttgttgata gtactcgcga gctttaattt ttttttgtaa ctggcggaat	420
cagatcttat gcaatactca aatccaaaga aacagtcaat ccagatgaaa ggcagtgaat	480
cgctagtttt cataaacaga atcatgttac tagtcatatt ttctataaaa attcaatact	540
tcattctttt tgttcaatac taactataaa tgcttataaaa tagattcaaaa tttcaaccag	600
atccaccact tcattaggct caaccaattc ttcataaata gaaacgtctt cctcagccaa	660
gcttaattga tgggaaaccc tagcttgcac tgaaggaaaa atacataatc caaataanca	720
actgtctttc caaatattct caaaattcaa cttcacgcgc tttcaccaag caggatctcg	780
tgattggacc aattctaatt cagaagttct tctcacacaa gtccgaacga ctcgatccat	840
cataatggat acatcggtca cgttgccacc aaatcgaatg actctgtttg cacctgtaca	900
aagtagaaca tatgcatgga aaagtaaaac tagtaaaacc gcataatgaa accaataatt	960
catcatatgt tgattgagtc tgaaccccat caaatataaa acaaaagtga gtttaaccat	1020
agttataaga agcagctctc cgttggtgta taatctatcc ataagatcgt caatttcagc	1080
atcttcaaca tcaatgttat tagcgtcacc tggaaaggct tgttcattag attctgattc	1140
caggtcacta ccaatatcat acatcattac tagtactttt tgaatcaatg gctcaccaga	1200
agccagttta aacaccttgt gaacttttgc tgcaccataa ggaccgagta gtagataagg	1260
atcgtgcaag ccgttatcca caacaatgca ttgtgctgta cccaagctta ctttcttcac	1320
aatattgtct actttcaaag taagttcata ctcaacatta gacaagtcac cctgtttcac	1380
tagaattttt ttccctgaat gctgttcaac catagtatcg tacgatgttc cctccatttc	1440
ccatgtggat ccaccacgta cctgaatact ggcagggtta atgggggtcta tgttaggagt	1500
tgaagactct gatggattat tgacaaatgg aatagagtct tgttgacttg gcaccagcgt	1560
ttcataattt gaagggtgaag gtactgggtt agccgagggt ggtgatgttg aaatatcact	1620
atcaattcct tgttctgagg atgagctagt agcagttgga tttgttggtc ttcttgacgc	1680
agacaaatct gatgttgatt ctaatggcac tgaattcgac agcgccaaat tgggttgctg	1740
taaagagtca ttggtggcag ggagaaatct aaatctatca tttgactgaa agtccttcca	1800
aaattctctg ctcaacaacc caccagttcc atttacatgt tcatgctttg taagtttcaa	1860

ttttatgaca ctgttattct gttccaaaag ctcttgattc aatcccaaca attcataaac	1920
actagcttcc tcttcttgaa atgaggttgg tattatattc ccttcgtatg atagttttat	1980
ttgttctata aatgtacgtg tgacagaacc ttcgtcattc ttagctatta ttaattgctt	2040
gagttgctta accgtagttc ggtcatttat ttcaatcatt gacttttcat tctgtaaatt	2100
aggaagattt gactccaaca aaaccggaa tcttttgaaa ttactattca tttctaaagg	2160
tttgggttgt gtgattgaag ctaatgggtg gtgtactaag tggtttttca attataaata	2220
ttgatgaact acactatata tacactgaga aaaacacgac caaaattgac accgcactaa	2280
aaacacggaa ttaccgtatt ctttttggtta acgattttgt ttcattacac gactgtcggt	2340
atacacacat ttagagcaaa ttattttaga ttgatcagtg ttagcaactg gctatcgata	2400
atagagtacc ttcccaggtt agaatgtctt attagaacaa caattgtttc atataaattt	2460
gtcgcaaagc acacgtaata tactatatgg aaggggctaa gtaaaaatgt cccgtttctt	2520
cttaatatga gaactcgtgt acgacacaat ttgctgtgtt gttaatcgag tatgtacaa	2580
cctgaaaatg gaccatagac ccaaactact tctctctttc tagcaccaca aaccacaaa	2640
ttagcacaac aatgaattgg acttcacttg tatatctatg gttcattttc aaaagcatat	2700
ttgctgactt aacatcacac caactcaaga gcaaagtggg attcctagat actactatcc	2760
tggatgaagt ggcccgaagc tatttgggat cagaggacgg aaatgttaca catggtaatt	2820
atgaaatatt gtcaattgca aatgggcgcc aatgacggaa acatcacatc atatttatgc	2880
cagttgccaa gaaccaaaaa aatggcacca acaaaacca agcccaccat gtcagttcat	2940
gaattgaaat cgcgagctat tgacttgata tcggaatcct ttgtcgaagg taccagttgc	3000
gtattttctt tcaacttgca tgcaaattat tggactatag gctattgcca tggaatcaac	3060
gttattcaat tccatgagaa tttggatgat ttataagcg gaattcataa accccattct	3120
ccaaatcatg tatatacat aggcaatttc ctgaagcaaa cactgccatt agaattcgag	3180
tttgatacta aagaacgcac aataagtcaa agattgtag gagaagtttg tgatttgaca	3240
ggagaaccac gtaccattga caccatttat agatgtgacc atatacttgaa aattgttgaa	3300
ttaacagaga taagaacatg tcaatatgag ttacacataa acgttcctaa gttgtgcctg	3360
ttgccggaat ttaaaaggac taaccttgaa gaaggtgtct cagaaatact ctgtacaaga	3420
attgaataag cattaaattt aataaaaaac atcaaaaagt gtatgtcaaa gtatttttac	3480
ctttgtaatt agtagtttgt cagtttctat ataaacatag ggtagttcgt atatacgata	3540
tcggagcgat tctaaataag tcgtggaaat tggccgacaa tgggatttga attttacttg	3600

tgtgtgtgtg tgtgatctga ataatagtag tgctaaacaa cttaaattaa agaaaaaaag	3660
acaaaacaaa aaaaattaaa tctgcttatt gaaaattttt cgaaataggc taaccctgt	3720
ttattagata ttagatagta cgatttggtc aagtggtcaaa gatagcaaat ttttattggt	3780
tcttcttttt tatatacagc ttgttttaat ttcaggatca ttttacacta acctactcat	3840
cagcctattt taatttatcc ttttggt	3868

<210> 112
 <211> 469
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 112

taacgaatga atataaaata cttgtattat gtagtgcaa taaaagttga aacgggtcgca	60
ctacttttta gtctgttgg tttgtgcact attttgtgtc agaaactgat ctatgaaaat	120
gatggttatt atgagaatgg aaaacttttc catcacacat caggtgatga cagaactaaa	180
ctatattgta tagtataaat aagggtatga aataccaaca tcccagaata ttaattatat	240
agaagggaag gagttttaat atatatcttg tgaataacaa cttcggtcta attcactata	300
cacaactagg cgtgtacacg ctcaatctca agtaaagaaa gtttatattc catcaagtcc	360
catctgttaa atatttttgt atctttttat ttttattttt ttttctttta atttcattta	420
catacattaa cacatctact aaccatatat cagcagatac aaaggcaag	469

<210> 113
 <211> 4545
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 113

tgacgatcct gtatatttcg tcataattca cacattctta aaattatgca cacatccttg	60
aaatgtgtta atattcccaa cattatcaat tatatgtgtt cagaattggg tgcaaagtta	120
tcaactcaat tcacgtata taaaccttac aaattctcta catttttata tttttttata	180
ttggcttttc ttttagaatc aatcaatact ttttttatca ttttagataca tctttcatct	240
attaatagat tatctttcta tatatcaaaa cagcacacag tcacgtgcca aaaaggatat	300

aagaaggaac ttcagaaaat taatcttctg attatactac ttactagatt gcataaagtc	360
aatatctgat tgatacaact tggttcatta ttcataaaac ttaacaacta attcaacaag	420
gaaaccaac aaaaaaatcc aaataaaata atcaggaaaa tattataatt aattaattac	480
aaaaaaaaac aaaaaaatac acacacacat acacacacac aaaatcttgt tgcaaaaaaa	540
aaaaaataat aataatataa taagaattaa ttaacaatgt cgtttccacg gacacattca	600
ccaagaccat ctggttcacg agaacaggaa gatctcacac tgatgattaa agcttttaga	660
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<210> 114
 <211> 916
 <212> PRT
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<400> 114

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 Gln Glu Asp Leu Thr Ser Met Ile Lys Ala Phe Arg Asp Ser Met Glu
 20 25 30
 Ala Lys Leu Asp Leu His Ser Gln Lys Leu Thr Ala Leu Val Ala Asn
 35 40 45
 Ile Pro Arg Thr Asp Glu Gly Phe Glu Asp Leu Ser Gln Arg Ile Thr
 50 55 60
 Val Leu Lys Asn His Gln Lys Ala Phe Leu Pro Lys Gln Glu Lys Glu
 65 70 75 80
 Ile Gly Ser Leu Leu His Arg Gln Arg Glu Glu Glu Gly Asp Ile Lys
 85 90 95

Asp Phe Lys Thr Val Val Gly Glu Glu Lys Glu Glu Leu His Gln Val
 100 105 110
 Glu Asp Phe Val Leu Lys Asp Gln Glu Glu Leu Arg Asn Val Glu Lys
 115 120 125
 Lys Val Leu Lys Glu Glu Glu Glu Leu Gln Lys Val Glu Glu Ser Met
 130 135 140
 Glu Lys Glu Lys Gln Glu Leu Tyr Gln Val Glu Asp Phe Ile Leu Gln
 145 150 155 160
 Arg Asp Glu Thr Val Lys Lys Leu Gly Glu Ser Asn Gln Ser Gln Gln
 165 170 175
 Glu Pro Tyr Thr Pro Ala Thr Ser Gly Ser Asp Gln Arg Phe Arg Ser
 180 185 190
 Gln Gln Pro Asn Ile Gly Asn Thr Leu Ala Gln Asp Leu Ala Leu Ile
 195 200 205
 Pro Lys Leu Asp Ser Glu Ile Cys Lys Ile Ala Val Lys Tyr Pro Lys
 210 215 220
 Leu Phe Glu Thr Lys Leu Arg Pro Pro Pro Pro Arg Asp Phe Gln Tyr
 225 230 235 240
 Lys Ile Gln Leu Thr Asp His Thr Gln Ile Tyr Ser Lys Pro Tyr Lys
 245 250 255
 Cys Asn Gln Glu Glu Gln Ala Leu Ile Lys Asp Phe Ile Asn Glu Lys
 260 265 270
 Leu Glu Ala Gly Val Leu Val Pro Ala Pro Ile Asp Ala Trp Leu His
 275 280 285
 Pro Ile Phe Pro Ile Arg Lys Thr Asn Ala Asn Gln Ser Ser Thr Lys
 290 295 300
 Ile Ala Val Asp Leu Arg Arg Leu Asn Lys Val Thr Val Arg Met Tyr
 305 310 315 320
 Thr Tyr Pro Thr Asp Thr Lys Asp Leu Leu Ser Ser Leu Thr Asp Ser
 325 330 335
 His Tyr Phe Ser Ala Leu Asp Leu Lys Asn Ala Phe Tyr Gln Val Ser
 340 345 350
 Ile His Lys Asp Ser Ile Lys Tyr Phe Gly Ile Ser Thr Ser Glu Gly
 355 360 365
 Asn Tyr Cys Phe Thr Thr Leu Pro Phe Gly Ala Ile Asn Ser Pro Thr
 370 375 380
 Ile Phe Thr Asn Phe Val Arg Gln Ile Leu Glu Gly Ile Pro Cys Ile
 385 390 395 400

Phe Ile Tyr Met Asp Asp Ile Leu Ile His Thr Lys Thr Leu His Asp
 405 410 415
 His Met Ser Leu Leu Arg Arg Ile Met Glu Lys Leu Asn Glu His Gln
 420 425 430
 Phe Gln Met Asn Tyr Asn Lys Met Gln Leu Leu Thr Thr Lys Ile Asn
 435 440 445
 Phe Leu Gly Tyr Ser Ile Gln Ala Asn Lys Ile Ser Pro Asp Ile Ser
 450 455 460
 Lys Ile Gln Ala Ile Gln Asn Trp Glu Leu Pro Thr Thr Thr Thr Gln
 465 470 475 480
 Ile Arg Ala Phe Val Asn Phe Ser Asn His Phe Arg Ile Phe Ile Pro
 485 490 495
 Glu Ile Ala Lys Phe Thr Asn Pro Leu Asn Glu Leu Leu Lys Asn Asn
 500 505 510
 Asn Gly Lys Asn Ile Lys Ile Glu His Thr Gln Ala Ser Ile Asp Gly
 515 520 525
 Tyr Lys Ala Leu Lys Ala Ala Ile Ile Gly Leu Pro Thr Leu Gln Leu
 530 535 540
 Tyr Asn Pro Lys Leu Pro Thr Ile Ile Phe Thr Asp Ala Ser His Met
 545 550 555 560
 Val Val Gly Gly Tyr Leu Cys Gln Pro Thr Phe Arg Asn Asp Lys Glu
 565 570 575
 Val Leu Val Pro Ile Ala Phe Ser Ser His Lys Leu Thr Glu Thr Gln
 580 585 590
 Ser Arg Tyr Ala Ala Met Glu Lys Glu Leu Leu Ala Ile Ile Val Ile
 595 600 605
 Leu Glu Lys Phe Arg Tyr His Cys Ser Asn Thr Val Glu Ile Tyr Thr
 610 615 620
 Asp Tyr Gln Ser Leu Ala Ser Tyr Leu Asp Lys Lys Thr Thr Pro Pro
 625 630 635 640
 Pro Arg Ile Ala Arg Phe Leu Asp Leu Ile Gly Ser Phe Ser Pro Lys
 645 650 655
 Val Tyr Tyr Leu Ser Gly Lys Lys Asn Phe Val Ala Asp Ile Ile Thr
 660 665 670
 Arg Tyr Gln Thr Gln Asn Ile Lys Glu Leu Val Asp Glu Asp Lys Ile
 675 680 685
 Leu Gly Gln Thr Phe Thr Val Lys Arg Asn Leu Lys Gln Gln Leu Leu
 690 695 700

Pro Arg Leu Glu Ala Ile Glu Leu Glu Asn Leu Asn Glu Ser Gln Val
705 710 715 720

His Lys Ile Gln Thr Ser Leu Glu Gln Gln Gln His Asp Leu Glu
725 730 735

Asp Asn Asp Glu Glu Leu Pro Leu Gln Ser Phe Lys Leu Met Asn Asp
740 745 750

Glu Leu Phe Val Ile Ile Asn Asn Gln Leu Leu Lys Tyr Leu Pro Arg
755 760 765

Ser Glu Tyr Asn Asp Ile Cys Gln Thr Ile His Asp Lys His His Pro
770 775 780

Ser Thr Arg Val Thr Asp Tyr Leu Cys Thr Leu Ala Tyr Trp His Pro
785 790 795 800

Asp His Leu Leu Ile Ala Thr Asn Ile Thr Arg Lys Cys His Tyr Cys
805 810 815

Gln Leu Asn Thr Ser Ile Arg Glu Ala Ile Arg Pro Tyr Arg Pro Leu
820 825 830

Glu Pro Leu Lys Ala Phe Ser Arg Trp Gly Met Asp Tyr Ser Gly Pro
835 840 845

Tyr Phe Asn Thr Val Gln His Arg Tyr Ile Leu Val Ala Val Glu Tyr
850 855 860

Val Thr Gly Leu Thr Ile Ala Val Pro Thr Leu His Lys Asp Ala Asp
865 870 875 880

Asn Ala Ile Ser Leu Leu Gln Ser Ile Ile Ser Ile Met Ser Ala Pro
885 890 895

Thr Glu Leu Val Thr Asp Gln Gly Lys Lys Ile Phe Ile Thr Ser Phe
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Gly Tyr Pro Met
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<210> 115

<211> 253

<212> PRT

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 115

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Ala Thr Pro Thr Ile Phe Asn Tyr Thr Pro Leu Tyr Leu Ala Leu Gly
20 25 30

Ile Glu Pro His His Asn Leu Asn Gln Leu Gln Lys Asp Leu Ile Glu
 35 40 45
 Asn Leu Gln Lys Glu Leu Pro Pro Glu Val Gln Ser Thr Glu Glu His
 50 55 60
 Glu Glu Asn Pro Asn Asp Glu Gln Gln Glu Glu Gly Arg Glu Gln Gln
 65 70 75 80
 Ile Ser Arg Glu Glu Gln Gln Asp Gly Arg Asp Leu Val His Leu Arg
 85 90 95
 Ile Tyr Glu Leu Glu Ala Ile Lys Lys Ala Arg Lys Leu His Thr Asn
 100 105 110
 Leu Lys Thr Arg Arg Asn Ala Val Gln Asn Met Leu Lys Glu Pro Tyr
 115 120 125
 Gly Ile Pro Ala Pro Phe Thr Lys Gly Gln Trp Val Tyr Arg Ile Arg
 130 135 140
 Ala Lys Ala Arg Lys Tyr Glu Pro Asn Phe Asp Gly Pro Tyr Gln Val
 145 150 155 160
 Gln Glu Val Leu Gly Lys Gly Ala Tyr Lys Leu Arg Asp Ile Thr Gly
 165 170 175
 Arg Glu Lys Gly Ile Tyr Asn Gln Asp Gln Leu Lys Leu Ala Tyr Ser
 180 185 190
 Ala Asp Asn Asp Pro Ile Gln Val Phe Ser Ser Phe Asn Lys Glu Tyr
 195 200 205
 Asp Arg Val Gln Gln Lys Leu Leu Asp Lys Ile Gln Ser Glu Arg Asp
 210 215 220
 His Gln Leu Asn Cys Leu Ser Val Gln His Leu His Arg Gln Arg Arg
 225 230 235 240
 Leu Leu Asp Ile Ser Ser Cys Leu Glu Gln Ile Ser Gln
 245 250

<210> 116
 <211> 2093
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<400> 116
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 tacattctga aattagaaaa atcattgata aattaattaa atttactact ttaactcaca 180

cacctaataaa ccttaataa attttaatta ctgaagtcaa attagataat aaaaccgaaa	240
tttatgttag tgattatgct tgttcatttg gtcgtgattt taaagctcaa ttatcaacgg	300
tggttttatt taaaataatc aagaaaaata atcttaaatt gaaaaattgg gataaaattg	360
tggaattat tgaaaaatta tatcaatatt cattgattat tgatgagaag gataactacta	420
ctactactac taccaatgat aataaggaag gtgatgatga aaaggataat aaggaagcca	480
ctgttgagac tgacaactca atattgaaat tattgccttc aaaagatatt aaaaaattcc	540
ctattaaaag aataactaat gatctgtttc tttcaatatt gaaaaattta attgataatc	600
aacctactga agaagaaatt caatcaactt tagcagctat ggattgtatt aaatcattag	660
atatcttgaa tgtattaaga attgttgctg aatccaagaa acaagctaac taaatctaaa	720
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aaggatataa gaaggaactt caccctctg ctcttcttat tattgtgtgt ggtgtaagtt	1860

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 ctaccgtctt tcaagcaaac ccaagtcgta ttgctcaaca ccaaaccag cggtttgagg 2040
 gagaaacgac gctcaaacag gcatgccctc cggaatacca gagggcgcaa tgt 2093

<210> 117
 <211> 2099
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 117

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 tactcggaat attactcaac atattcccaa aataatcgta aagataaatc tttgagagtt 240
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 gttcgtacac atgatgcaac aactttctag tacctacttg cacaaagtgt agtttgcaaa 360
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 ccgatgggtca tgcaagtatt cgcctttctc ttttgtagat ttatgtagtt tcaagatgac 480
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 aacaatataa acgagggtgtt ttccttttct ggtgcttgat ttgaaacgtg tacattccct 720
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acagggattt tccaattcac atagccaaaa gtatttttgg tttccacatt ctttcaaaac	2040
aatatttgtg ctacctcccc cttccacca aaagtatccg attccaacca taaagcagc	2099

<210> 118
 <211> 3284
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<400> 118	
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attaggtaca aatccaattc tgtagctctc atcatcaatt cttgagactc caatcacca	180
atttaactca tctgaatgat acaatgtatc aatattctga aaatctaata aaatttcaat	240
attatcgccc tgtttaaatg acaaatcacc tgggtcataa ccactaaaat cgtattttgc	300
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<210> 119
 <211> 791
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 119

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gttaaactag atgtaccaat attagtagga taaataaaga atcaataacc atggcacgtg	180
aatatgaaaa ggtaggggct aatataagtg taagtgtagt gtataaatta caaaacaaaa	240
aaggctgttg ttattaagat gagtcaactg tgtaagtgac gatcctgcat atttcgtcat	300

aattcacaca ttcttaaaat tattcacaca tccttgaaat gtgttaatat tcccaacatt	360
atcaattata tgtgttcaga attggttgca aagttatcaa ctcaattcac gctatataaa	420
ccttacaatt tctctacatt tttatatttt tttatattgg cttttctttt agaatcaatc	480
aatacttttt ttatcattta gatacatctt tcacttatta atagattatc tttctatata	540
tcaaaacacg acacagtcac gtgccaaaaa ggatataaga aggaacttca tcttgattgc	600
gccgcaagca acaacaata agccaaggaa agtatatact ccagatctac tatgagtatg	660
acacagctta ttaatgatca agtctacaac ttctactact aaacacgttc ttaacaaatc	720
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agctaattct a	791

<210> 120
 <211> 4581
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

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aagactacaa cttaataaaa atgggatatc caccaaattt caaaattggt actaaatcat	180
taacagaaaa cattttatta gcatcaacgg ctttttcaag agttgataaa ttcaattttg	240
gtgctcgtat ggcggtattt aaatttcctc aatcaaataa aatcatttta tggtcaccat	300
taccttatac accacaagta attgatgttt tgacaaaatt taccaataat accaatgaat	360
caaattttaa tattgcttat gtgataattc ctgatcgtga acataattta gctgctaaat	420
catataaaga aaaatttccc ggggtgtaa taattggaat ggaaggatta gatgaaaatt	480
cattgaaatt ggattataaa ttataaaaac tgatgggtaa taaagtttta aaaaatgatg	540
aattaaaaca aatctttaat gacagtgaca gtggcttgat tgttgataat tttgaatttg	600
tttatttacc aatcatgca aatcaagaat tgggtgtatt tgataaatca tcatcaacat	660
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ggtcatttat aactagatat ttacaacat attctaaagt tggtcgtttc ttatttagaa	840
aaattgttga tataaatcat agtaaactg gattagaagc tattttataat tcatgggatt	900

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tatttttactt tacttttactt tatatgatat tataatctgta ttaatgacga actgaaattg	4500
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tgatgtgggtg gtgtcatatc a	4581

<210> 121
 <211> 5325
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 121

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caatcaaact aatctttgca ctgcggtcaa aatccaaact aaagattcat tccatagatg	180
ttaccacagc tttcctcaac ggggaaatac tggaactcat atttggtgaaa caacctccgg	240
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gaatgattga ggagttaaaa ttatctgtct cagaaacaaa cccagtatct ataccatctg	660
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ccaaataccg aagtttgata ggcaagctct tgtttgccag taatactata aggtttgaca	780
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ccataaagga agccctttgg ctaatatata tttttcgaga tattaatgtg atattgaaat	1140
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<210> 122
 <211> 2027
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<400> 122	
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tatcatccga tccttaatca agtctattac tgaatatcaa ttatttggac acctgtttat	180
aaattactat ccaatctatg ttctttcaat tctttccttc aatattttgc cagccaataa	240
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aattggaatt gaacaaagtt attaattact gaaaaaggaa atttaatttc ttgaaaggca	1140
aatctttgtt tgtttttttt tttgggtctt ttctttcatt taataagcgt ggggtattaa	1200
tagataatga tattgttggt gttattgtga tattgtgtg aaatttgaca tatgataaga	1260
taagtttctt tcttttctt caactagtat aattgaacta aagaccacca ccaccaccac	1320
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attgtgcaca ggtaactac cttaatatag ttattgttaa tacagttatt gctgttgact	1500
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aactaccgta ttaaattatt gtattaagat tgattcctat taaggataaa acagagagt	1620
tgtagaaaag agaaagggtg gattataaat atgtgtaaaa tcccccttag agactaacca	1680
ctagaaatct attgatgggt tcatatatag agattaacga ttatatttat aatataagtt	1740
ggtagttgct agtatatttg aaagcactac agtatagtat gtcagaatca gatcatttaa	1800
actctactaa taatacagga aacactttca ttagtctaga tcaagccagt acaataatgg	1860
cagatcaaac tcaaggagct aaccacaaac aatgataatt catctttttt gtcaagacga	1920
taggttaatg ttacaagcac tttattgggc tcgaaatagt ggtaaataag tccatagata	1980
tgacctgtta caagttattt cgatgatcaa gccggctctg tgattac	2027

<210> 123
 <211> 2118
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 123

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atattgctga tagatggtga aaaaaaaaaac ggaagaatgg ggatagcaaa actgtgggtg	180
agattaactc atctatggcg ctaaaagtct ttttttttc tcttttatta gggggcacat	240
aaattattct tttcattgat aatctcgagt ccgttttttag ttcattattc ggaatatatt	300
accgtattgg gaacgataat tattattagt tctcccgat gggtcgattt tgctgggtgca	360
aaaatataaa tccgatatta ctttattggt gttttaataa atccgtttta aaagtccgta	420
gacatatata ggatgataat aatttaaccg atttataagt tggaatcatt tggatgaatc	480
cgcttgggga gacgttttcc aattttagaa gtttaactat caattttatg tgacatccga	540
gtgtacacat tttgtgaatt tgatcttatc aactcacttg gtgtaccatg gcatttataa	600
caacactttt tagaatcggc tgagttacat gcatttcctc tatttgtaga ttaatggaaa	660
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gactaaaaaa taattgatat ctctaatacag tgacagctct agtcaacttg accgtaatgt	780
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gatcaattcc cgtcaaaacg catttggcac ttaatctttg attgaaccga ttttgatctc	900
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cacaacaatt accatattat atgaagaaga ctataacaaa actgtagata gtaggggatt	1980
ggttatttcc ggggagtaga agtattgggt tatctaagtc aatctttaac aaccaacaat	2040
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<210> 124
 <211> 4929
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 124

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agtttctgat caagaaatat tagatgcttg ggaaaaataat caattggata ggttttcagt	180
ggatcaattg aaggcattta gaagaaaata tcttgatgtc aaatcagcta ataagaaagc	240
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atagtgatat gtttatagct ctgtaaatac atgtaaattt tttggttgcc aatgaattga	360
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aggcagttac ttgtttaaag aagtgatgag tcgtgattaa gtaaagtttg cagcactaaa	480
tattgtatgg tatttgactt aattttttct gcaaaaaaaaa ttacaaattt ttaatgaaaa	540
aacaaaacac aagataataa cattatagaa taaagattat aggatcctac caacatagtt	600
ccattgctga tcaggacggt taataaaaga gcttcccaac agagacatat cttaataata	660
acaggctatt ttctgccttt aaaaagccat ctaggctcaa aaacctcaaa ataattcatc	720
tcccaccttg gcagcagagt agccataaca cagccaaatc aatttctata gtttacataa	780
tatataaaag gtttctaata gccagtaagc ttatagaaat tacccttttc aagtgatttg	840
atgaacaaat tatattcttg tacaaaatag tatatttaaa attaagaatt tggcttgcaa	900

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<210> 125
 <211> 4954
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

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attattatta ttatgacata atactacttg aataacagtg aactgtaatt gtattaagaa	180
caaatcataa caaaggaaga tgatgacgat gatgatgacc ccttgaaata tccagggcac	240
atgcattgtg atgattgttg taatatagct aatgctaatt cttgattagt gtggaaagcc	300
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tgaaaaccaa ctaactaccg tattaaatta ttgtattaag attgattcct attaaggata	480
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agagactaac cactagaaat ctattgatgg tttcatatat agagattaac gattatattt	600
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cagatcattt aaactctact aataatacag gaaacacttt cattagtcta gatcaagcca	720
gtacaataat ggcagatcaa actcaaggag ctaaccacaca acaatgataa ttcattcttt	780

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<210> 126
 <211> 1047
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

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tctaaaatgc atatggcaca atgatctcac ctcggttggt taaacctttt tcttcttatt	900
aatcttatct tagttgtagg ttggtctccc cccoctaact agttttacaa ttcaattatt	960
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 <211> 7929
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

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<210> 128

<211> 2292

<212> DNA

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 128

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tggacaatta attgattgat taataaattg gttttattag tattatgtaa gggatttcaa 180

agaagtcac taaaaattgt taatgtagat gtagatgtag atgtggttgt tgttctatgt 240

gtttacagaa attgatcac aaagtccaag attttacatt gcctcgccag ttctattttt 300

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tgaatgcgga agaggaagga ggtcattcca ttccattcca tcgcctcatt cttctccatc 420

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acgtgccaat attatgaaat attccatttt gggaaagtca gcttcaatgg cttacatggg 540

agcgcatact catagatttt aaaaaatctg aataatttgt tagttctcta tgaatgaata 600

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gatagcaaaa gtattcatga attattcgta ttcgtaaaaa atttaagaag gagggagaac 720

aacaactgtt aacccaaatg gtgtttttgt taaaactcta tctactaaat tcaacatttg 780

tgaagataaa agtggttcaa attttttgta tgaaaaaaca acatagattt atatagcaac 840

atcactacag taatatatcg aatacaataa atatatatat ataataaatt aaaataaaaa 900

taaaaatata catctacaat atgaaaaaaaa tcatttaact atatagtatg tctaaattat 960

cgaatgaaag ttagtaatac aaactcccat gtttagtggg gagcttggtg gagccttcaa 1020

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<210> 129
 <211> 2025
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

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ttggatttgt cgggtattga aaccacaaaca tattataatt tgctatgcgt ttaaataaac	1920
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2025

<210> 130

<211> 2731

<212> DNA

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 130

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ccgcaattct agaaattcct ttttttcttt tctttttctc ggagttgggtt acaatacaaa	180
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gataaaacag agagtgtgtt agaaagagaa aggggtggatt ataaatatgt gtaaaatccc	660
ctttagagac taaccactag aaatctattg atggtttcat atatagagat taacgattat	720
atttataata taagttggta gttgctagta tatttgaaag cactacagta tagtatgtca	780
gaatcagatc aattaaactc tactaataat acaggaaaca ctttcattag tctagatcaa	840
gccagtacaa taatggcaga tcaaactcaa ggaggttaacc cacaacaggt tatgagcctc	900
gcccgttat tgaatttaga taatataggg gcaatgaaag cttttgaaag tgttgatttt	960
cctgaatcat taaaactaga atccaagatt aattttcaag tgtggagaaa tgaaatcctt	1020
agatatgcac gtggtattgg tgctgagttt gaaaactttg tattgaatga aactccagct	1080
cacctgtatg atcttagatt gggaaatatg cttcatcaat tattgattcg cactgtgaaa	1140
gaaaaagtta gaatgcctag gcaagaactt ggaaaatcag gaaaagaact ttatcttgat	1200
cttattaaat cattcggtac tcaataccca tacgataaat ttgagatagt taaatactat	1260
tgggatcagt taacaaaccc ttttaattaat gtgaagagac gttttgaaat tgaagaagta	1320
tgggttcaat acattaatgc tcaaactgca acagagagag aagttcttaa ttcatttggt	1380

tggttacatt tgtcaaaatc tatattacca caagagtacc ttagaagtgc ccatccagtt	1440
cttgataaaa atgtgattaa aatatttctt gataccatc caaaatgtga tattgatcaa	1500
attatgtcat ttgtaaataa tgaactgatt aattatgtag ggaaaaatga tacaagggaa	1560
aatgatatgg gacagaatth aagagagagt gatttaagag agagtgactt aagtgaaaat	1620
gatatacaac aaaatgagtt aagcgaaagc gattcaagtg aaaatgattt aagagaaata	1680
gcaacaaaag aaactgttag tgaacttttt gaaaatcaat gtcagaattg ttttggactt	1740
ggatcatgatt catatgaatg ttcactggca tttagaaaca atcagtatat tccagattta	1800
ttttctagac ttcagagttt tcgtggaaat agaattcaaa ataataatag aaatgtctgg	1860
tctagattct cagaacaaga tgagtcaatt gcaatacag aaaaaggtaa ctagatctaa	1920
tgataaaaat gaaaatcagt ggcagtcaaa acaatttaca tattaacaa gtttgaatgt	1980
aagttgttgt tgtttagata aactatgtca tggatccaa agttttattt tatatttatt	2040
atttaagtgg tcatgtttat ttacttataa ttgttattta gtttttcaag tgtgaatttt	2100
acttacttat aattgtattt agttttcaag tgtgaatttt acttacttat aattgtcatt	2160
tattgttcaa gtgttatttt tacttactta taattgttat ttagttttca agtgtgaatt	2220
ttacttactt ataattgtta tttagttttc aagtgttata ttacttact tataattgtc	2280
atttattgtt caagtgttat tttttactta cttataattg ttatttatgt gtccaagttt	2340
taatattatt tacttataat tgttatttat tgtatatgtg ttaatttaat tcaattgtta	2400
attgttattt attgttcaag ttttaatttt atttacttat aattgttatt tattgtttat	2460
gtgttaattt aatttaattt aattgttatt ttactattt aaatgttgat tttatttatt	2520
taatgttaac ttgtcatttt taattttact tattatattt tacgtgtgac tattatctat	2580
gataaaacac taatagtgga tattgagtgt ttatttggtt catcgcagag gatatttatt	2640
ggaggagggg gaaaatgtct atttggtata aggaagacca taaaagttgg ttccaaatag	2700
tcaaccaacc aataaacatt cctcatgct t	2731

<210> 131
 <211> 2858
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 131

cctccgggcg tctatttaca agctgcttta ttatttggtta ttacctgggt gtaaaagccc	60
tcttgcatth gagctatttc tattcccact tcgggtatttt ttttacagcc tcgttagacg	120
agttcttgat attactaaat tagttgttta ctgagtggcc tgatgggtcc tcgtcactct	180
agtttttggg ctatataagg gtcagaaatt tcccttctcc ttaggtccat caagtcaaga	240
tatacattag ttggtagcat cgtatggaat tttcgtatga acggcatacc aagtattaat	300
ttccgatcga aatttttttag gacgtcttga taatcaggac aaacatcatg aaaggtctat	360
acgacgaaag tttactttac acaaggggag accatatgtc ttctttatta acaactagtt	420
atatagcgaa caaataagtt tatacagaaa tatatgtaca caaacaagt tattgtttat	480
taattattta attagctcgg aagaataact ctgtgatact gcatacattc aaacaaaatc	540
aatctagttt ccaacatctt tttcacttgg taatgtaatt attcttggtc tggcaccgac	600
aatgggtatt gttttgtagc tggaggacta atatggggta ccacctcaat ttttggatcc	660
cagctcccac gcaggggtgg cttctgatct aactcacttt cgaaaatata ctgatagttt	720
ccaattaatt cagcaaaaata gctcttggtt gtacccttaa ccaatgacat gatatccttt	780
ttattatcac cgataccacc tgtgtcttcg tcttggttga atatagctaa tgctaattct	840
tgattagtgt ggaaagccta ataaggttat attgtgcaca ggttaactac cttaatatag	900
ttattgttaa tacagttatt gctgttgact actattgtta ttgttaaatt aaagtgttag	960
gttgagttaa ttgattagtg aaaaccaact aactaccgta ttaaattatt gtattaagat	1020
tgattcctat taaggataaa acagagagtg tgttagaaag agaaaggggtg gattataaat	1080
acgtgtaaaa tccccttttag agactaacca ctagaaatct attgatgggt tcatagatag	1140
agattaacga ttatatttat aatataagtt ggtagttgct agtatatttg aaagcactac	1200
agtatagtat gtcagaatca gatcatttaa attctactaa taatacagga aacactttca	1260
ttagtctaga tcaagccagt acaataatgg cagatcaaac tcaaggagct aaccacaac	1320
acgtcttctt cagtattagg gaacaacata ctaacttgac cttttctagc ttcaacaaaa	1380
aattcctcta tatccattaa tggaatttca tcaaactgag cagcccaaaa aaacgttttg	1440
cttccaaagt ctaaagtgc atggaatttc cttatgaaag gtataccaag tattaatttc	1500
ttatggaagc tgtccactac agcaaaatcc tcttggaatg taataccatt aaactggaac	1560
ttgaggttaa ttatttggtt aaagtttctg ttgatttttg gtccaataaa gtacccaaac	1620
tactagagct ccaacaacat tttcagaaaa tggccaataa tacaataagt gggatatatt	1680
tatcaaaaga gtttatatta tggttactcg acggtattat tctctgttga ttttaaggcat	1740

tctgggtcgac cagtggacaa aattcaagag tagtgtttgt ttagacttta caggacatga	1800
tagtatatat aacaaaaatg aaatacatta atcaaaaacta actaaatcct aaattaatgc	1860
caatttctat tgaattgggtt tgctactttg taaaatttgt gagtaatcct aagtacttat	1920
atggaaatca acaatggcaa aaatacaaga gaatgacccc atgacacatt cagtgcacaa	1980
ttcatagtaa ctgcttgggtc acttgacat gactctgcta gtatactcaa ccactcttgt	2040
gacttccata tagatactct cgatgaaatg tctcaaatta gaggacaaac aatctgctat	2100
aatcttgggt aatcacccat gtaacatgga ggaaccaaac acatagatat acggtaccat	2160
ttcatacaga atttatcact aaagaaatta agaaaaactt gtgttatcaa agtgggttgc	2220
gaactttgta gtaagggaga gtgttgagaa ttagagattc taagtccag aaaaatatct	2280
atatttatat atatataggt agtgcaacac tacataaaag ggactgattt gaatgtatgt	2340
atgtcaaatg acacccttat aatgttgagt gacatcatat caaaatggaa atctactgta	2400
tcaattaaga gattactaaa agcaatatac ttaatatgag gtcgtacttt aagattgtga	2460
atagtatcag tagcgagtgg ctatgtgttg tgatggagca tcaactgtag tttcttagat	2520
gtaaatctca gtgactataa gcatactaaa ttagttatga agatatgttc cattaaagta	2580
tttaaaaaat aatagacagg ctatcaattt ctaatatagatt taccgtccag attataaaaa	2640
aattatcgag atacatatta caccgattga attaataata tgtctactac aaacctatca	2700
cggaacttga tgcaattgat tgaataagtg tctctctaac gatgacatgt ccaattctaa	2760
tcaaaataat tattattcta attgtaatat ctggtattta attatttata attcacgaaa	2820
cagtttgatt ggtttctgat tcttctgaca aaaataag	2858

<210> 132
 <211> 1636
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 132	
atgtttatatt aataattaaa cccagttga ccaactatga aatagtataa tgataaatgc	60
aaaataaata tagtatgaac aatatgatag ttttagtggt aattttgaat aagaaaaaga	120
agggataagg atatttttac taggaaactc aattataatt actaatgata aaaactccat	180
cagctactat tattactcaa attttaaatc atttgtttat cacctacaca aacagggtat	240

gtccaatatt gattactaaa attagaacaa ataagagaat ataattgaag ttaaataatt	300
cttttactaa atctattgac caagaactac atcaagggaag agtggtgcat atacatctaa	360
tggtttattct tggtagagt attgatacaa aattatatca tcaccaacga atcacattaa	420
gggaaagtgt tgtgcatata cctgatgctt agtcttggtt aaagtatttg tgtgaaagg	480
tatcgtgacc aaagattata gtaagggaag gtattatgaa taaatccaat gtctactttt	540
acagaagtat tgacatgaga gattataact atcaagaatt gcattaaggg aaagtgttgt	600
aatatagcta atgctaattc ttgattagtg tggaaagcct aataagggtta tattgtgcac	660
aggtaacta ccttaatata gttattgtta atacagttat tgctgttgac tactattgtt	720
attgttaaatt taaagtgtta ggttgagtta attgattagt gaaaaccaac taactaccgt	780
attaaattat tgtattaaga ttgattccta ttaaggataa aacagagagt gtgttagaaa	840
gagaaagggt ggattataaa tatgtgtaaa atccccctta gagactaacc actagaaatc	900
tattgatggt ttcatatata gagattaacg attatattta taatataagt tggtagttgc	960
tagtatattt gaaagcacta cagtatagta tgcagaatc agatcaatta aactctacta	1020
ataatacagg aaacactttc attagtctag atcaagccag tacaataatg gcagatcaaa	1080
ctcaaggagg taaccacta caggttatga gcctcgcccg cttattgaat ttagataata	1140
taggggcaat gaaagctttt gaaagtgttg attttctga atcattaaaa ctagaatcca	1200
agattaattt tcaagtgtgg agaaatgaaa tccttagata tgcacgtggt attggtgctg	1260
agtttgaaaa ctttgtattg aatgaaactc cagctcacct gtatgatctt agattgggaa	1320
atatgcttca tcaattattg attcgactg tgaaagaaaa agttagaatg cctaggcaag	1380
aacttgaaaa atcaggaaaa gaactttatc ttgatcttat taaatcattc ggtactcaat	1440
accatacga taaatttgag atagttaaact actattggga tcagttaaca aaccctttaa	1500
ttaatgtgaa gagacgtttt gaaattgaag aagtatgggt tcaatacatt aatgctcaaa	1560
ctgcaacaga gagagaagtt cttaattcat ttgtttggtt acatttgtca aaatctatat	1620
taccacaaga gtacct	1636

<210> 133
 <211> 2125
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 133

tgagtagcct tttcttgggc gactttatta gcttcatcaa caagacgttt atcttcagct	60
tcctttttcca taataattct cttccattct ggaattgggt ttggtttctt tttatttatt	120
tcctcttctt tcatagccaa caaaagagta cccaataata atataatggg gataccttgt	180
gcgtacattc ttgcttgaac agctttttgt gcggtatcca taattttgtc tctgttaacc	240
aatacccaag aaccatataa ggaaccagcc caagcactta tgataatttt atattttattg	300
tcattcaata cggtgaaaca tttgtcacta agcgataatc tgttccattc acggtattct	360
tccaaatatt tagcttcttg atactccgat tgatgcatct ttctatcgaa ttcaacagaa	420
ccttgatcag cgaaaaaggc agccacagaa attggtggca tagcaattat ggctgctttg	480
atacttggat tgaatgttgc aaatcttgct ggatgtctat gctttaaata ttggtacaaa	540
cggactgaaa gtgcaccacc ataaaacaac ctttggcac cttctgaaat aatatgtgaa	600
atgtgagcgt ctttttcttc tttggataag atcttcattg tggaaattaag atgactttgt	660
gattaaattg ttgacttctt taagcctttt aatgtggagg aaaaagaaaa atctataatt	720
aaaaaaaaa aagataaagc agataattct ttgatcttta tatacttggg ctatatgtag	780
taggggaaag tcggagtcgg aatttgaaaa aaaaagagaa aaaagaacga atatttagac	840
tgtaaaattc aaaccctgc tgattagtat ataaaaaaaa tgagttcatt tttcctttct	900
ttttttttt ttcgcgcgga tagcaacggt cattaagtta acgagataaa aaagaaacaa	960
ccagataatt atgaaaagtt gtgatgggtg cacgtgcgaa catgagagtc atgaattttg	1020
acgaaaacgt caagcttcag tttacaaaag acctctttat taaaatcgaa ttgcttatag	1080
ggcgcgcgat gatgagaagg tgtatgttgt aatatagcta atgctaattc ttgattagt	1140
tggaaagcct aataagggtta tattgtgcac aggttaacta ccttaatata gttattgtta	1200
atacagttat tgctgttgac tactattggt attgttaaata taaagtgtta ggttgagtta	1260
attgattagt gaaaaccaac taactaccgt attaaattat tgtattaaga ttgattccta	1320
ttaaggataa aacagagagt gtgttagaaa gagaaagggt ggattataaa tatgtgtaaa	1380
atccccctta gagactaacc actagaaatc tattgatggg ttcatatata gagattaaag	1440
attatattca taatataagt tggtagtgtc tagtatattt gaaagcacta cagtatagta	1500
tgtcagaatc agatcaatta aactctacta ataatacagg aaacactttc attagtctag	1560
atcaagccag tacaataata gcagatcaaa ctcaaggagg taaccacaaa catagaatac	1620
gttttcaact acttaagtat ccactaacct aaattttttt tttaataaaa tttcattgta	1680

ttagtctttc ttactgcttt taatcaacta taagtatagg ttccggtttt ttttgagta	1740
aaatttatcg ttcaggagaa ataacaaaat gtacacgact ttttcgcagc attttttttt	1800
ttgttttggg tttttgtatc aaattgttac aacaacaaca acaacctcaa ttcttaacca	1860
aatctacccc tcctatTTTT tttttctata cacacaatac atcttacact atcttttgat	1920
aggctttatt gaagaagtat ttaaggagtg taatgacaat ctgcttaact catatatata	1980
tatatagata gtagtcaaca atagctttat ctactttttt tttttggcga ccctgcaac	2040
ttcaggccca ccagtttgcc ctttttggtg cccccattga gtaaactgag ggatttgag	2100
cacacttttt tttaggtaaa aatgg	2125

<210> 134
 <211> 1292
 <212> DNA
 <213> Unknown

<220>
 <223> sequence of retrotransposon from unknown organism

<400> 134	
ctaatacaaa aatccataac ccaactgctc aacggcgaaa tccaaaactt ccatgctatt	60
ctagacaaaa cagtgtcgaa actcaatgat gcagagtggg gtctcgccgt tatggttgaa	120
aagaaaaaga aacttgacga attgaaagtc aaagaagaag cggcaagaaa gaaggaagaa	180
ggggcaaga aaaaggaaga agaggcaaag aaaaaggcag aggaagcgaa gaagtgtttt	240
attttacttt tctgtcaaat ttgcactact ttttaattgt gtgcaaatat tctattttac	300
ttgattttta tatactttta tttacaata cttttttata ggacttttta tatcttttct	360
ttatcaactg ttcgctatag ggtaggctct ccaagctaatt tttaccgac acaagatgaa	420
atattttctg ttgagcactc gttgtcgaca gtgaaaaatt ttcactcaag aaaatatatt	480
atcatcactt tttctagaag ggagggtcaa gtgttggaga atagacagcg aacacctgat	540
attcccaagg tcgaattaga ttgaaagata aataatagtc atattttatt tgtatttagt	600
caataaatta tctttttata tttaaattct tagtattgtc ataccacgta gattgatagc	660
gacatactta gcacatttaa catatattaa gcaccgatta cctgtgacat tccggagtgt	720
actgtttcgc gcacgtggc agacgaacat caactcatct tttatacaat atattcttac	780
gattataact ttcaattaag aaatacaact tcttattagc attctcctac aagttcttaa	840
gttcctagga atttcttcga aactataatt aaagacgaaa agtgtaaaac aaacagaaag	900
cagaggaggc ccagaagaag gcagaggagg ccgtcccaca aaagtttgac aactttgacg	960

actttattgg ctttgacatc aacgacatgc agaacgacga taccatcgac gataccatcg	1020
acgataccat cgacgaaacc atcgatgaaa ccatcgacga taccaacgac gaagacatgt	1080
tgtccaacat ggactacgaa aatctagatc cggacgagac catcgacgaa gtacctgcca	1140
ccacagacag cgacttggac atgaacaaca tacttgaaaa caacgagctg atattagacg	1200
ggttgaacat gacattcctc gacaatggca acaacaccaa ccacgtaaac gaagagtttg	1260
atgtagacgg ctttttaaac cagtttggtg at	1292

<210> 135
 <211> 568
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 135	
gattgtatag tgggtgtggtt gatcgacttc aatataacaa gagagagatg agatgagatg	60
cttttatcgc gtatatatatt ttttttccat tgacaattct gatttcacaa attgttcgct	120
atagggtagg tcttccaagc taattttacc cgacacaaga tgaaatattt tctgttgagc	180
actcgttgtc gacagtgaaa aattttcact caagaaaata ttttatcadc actttttcta	240
gaatggaggt tcaagtgttg gagaatagac agcgaacacc tgatattccc aaggtcgaat	300
tagattgaaa gataaataat agtcatattt attttgtatt tagtcaataa attatctttt	360
tatatattaaa ttcttagtat tgtcatacca cgtagattga tacggacata cttagcacat	420
ttaacatata ttaagcaccg attacctgtg acattccgga gtttactgtt tcgcgcacgc	480
tggcagacga acagattaga agcttggtaa atctttgggtt attcatcacg tcttgagaat	540
aatacaaagt ttaatatagt attttcaa	568

<210> 136
 <211> 946
 <212> DNA
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 136	
gattgtatag tgggtgtggtt gatcgacttc aatataacaa gagagagatg agatgagatg	60
cttttatcgc gtatatatatt ttttttccat tgacaattct gatttcacaa attgttcgct	120

atagggtagg tcttccaagc taattttacc cgacacaaga tgaaatattt tctgttgagc	180
actcgttgtc gacagtgaaa aattttcact caagaaaata ttttatcatc actttttcta	240
gaatggaggt tcaagtgttg gagaatagac agcgaacacc tgatattccc aaggtcgaat	300
tagattgaaa gataaataat agtcatattt attttgtatt tagtcaataa attatctttt	360
tatatttaaa ttcttagtat tgtcatacca cgtagattga tacggacata ctagcacat	420
ttaacatata ttaagcaccg attacctgtg acattccgga gtttactgtt tcgcgcacgc	480
tggcagacga acatcaactc atcttttata caatatattc ttacgattat aactttcaat	540
taagaaatac aacttcttat tagcattctc ctacaagttc ttaagttcct aggaaattct	600
tcgaaactat aattaaagac gaaaagtgtg aaacaaacag aaagcagagg aggccaagaa	660
gaaagcagag gaggccgccc cacaaaagtt tgacaacttt gacgacttta ttggctttga	720
catcaacgac aataccaacg acgaagacat gttgtccaac atggactacg aggacctaaa	780
attggacgac aaagtacatg ccaccacaga caacaacttg gacatgaaca acatacttga	840
aaacgacgag ctgatactag acgggttgaa catgacattg ctcgacaatg gcgaccacgc	900
aaacgaagag tttgatgtag acagcttttt aaaccagttt ggcaat	946

<210> 137

<211> 951

<212> DNA

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 137

gatttgagaa ataccattga agatctagag ttaaaaataa ggaatttgca tgtacatgag	60
gataatcaag cggtcattac aatcttaag aatgataatt tccaccacaca tagaccgatt	120
gatatatgtt acaaatttct cagacaaaaa ttgaaagatg gatttttttc aatatcatat	180
gttgaatctg gagataattt agctgactca ttcacgaaag ctttaggaag aaataaattg	240
attgaacata ccaaaaggat tagagaaaga aaggattatg ataataatgc tacactgata	300
gtggacgtta ggacgctcga agagattaag ataaacaaga aattggtaca tcattaatta	360
atttagctgt ttacctgaat caggggagtg ttcgctatag ggtaggtctt ccaagcta	420
tttaccgcgac acaagatgaa atattttctg ttgagcactc gttgtcgaca gtgaaaaatt	480
ttcactcaag aaaatatttt atcatcactt tttctagaat ggaggttcaa gtgttgagaga	540
atagacagcg aacacctgat attcccaagg tcgaattaga ttgaaagata aataatagtc	600

atatttattt tgtatttagt caataaatta tctttttata tttaaattct tagtattgtc 660
 ataccacgta gattgatacg gacatactta gcacatttaa catatattaa gcaccgatta 720
 cctgtgacat tccggagttt actgtttcgc gcacgctggc agacgaacac aaatgcttga 780
 actatctgcc gacttttttt tatttatggc gtgagacatt gttctcgcac acggttgtga 840
 tttatctacc aggtctcat atttagagcg acaactactt tgagcaagca aaacgcatat 900
 ctcaccacac accaattgta ggtattctc aaccggaag tacaactagc a 951

<210> 138
 <211> 107
 <212> PRT
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 138

Asp	Leu	Arg	Asn	Thr	Ile	Glu	Asp	Leu	Glu	Leu	Lys	Ile	Arg	Asn	Leu
1				5					10					15	
His	Val	His	Glu	Asp	Asn	Gln	Ala	Val	Ile	Thr	Ile	Leu	Lys	Asn	Asp
			20					25					30		
Asn	Phe	His	Pro	His	Arg	Pro	Ile	Asp	Ile	Cys	Tyr	Lys	Phe	Leu	Arg
			35				40					45			
Gln	Lys	Leu	Lys	Asp	Gly	Phe	Phe	Ser	Ile	Ser	Tyr	Val	Glu	Ser	Gly
	50					55					60				
Asp	Asn	Leu	Ala	Asp	Ser	Phe	Thr	Lys	Ala	Leu	Gly	Arg	Asn	Lys	Leu
65					70					75				80	
Ile	Glu	His	Thr	Lys	Arg	Ile	Arg	Glu	Arg	Lys	Asp	Tyr	Asp	Asn	Asn
			85					90						95	
Ala	Thr	Ser	Ile	Val	Asp	Val	Arg	Thr	Leu	Glu					
			100					105							

<210> 139
 <211> 9850
 <212> DNA
 <213> Candida albicans

<220>

<221> misc_feature

<222> (1)..(9850)

<223> 'n' can be any nucleotide 'a', 'c', 'g' or 't'

<400> 139

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<210> 140
 <211> 305
 <212> PRT
 <213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 140

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Lys Leu Glu Asn Asn Ser Asp Ser Lys Tyr Gln Ser Leu Glu Thr Tyr	35	40	45
Ile Asn Ser Lys Tyr Ala Asp Thr Ile Lys Ser Phe Glu Lys Leu Lys	50	55	60
Tyr Leu Asp Ile Asp Asn Ser Glu Leu Val Asn Thr Trp Ile Met Cys	65	70	75
Phe Asn Gln Val Lys Arg Phe His Pro Gln Val Phe Asp Ala Phe Met	85	90	95
Glu Ala Glu Asn Glu Asp Glu Ile Gly Ile Glu Lys Ile Gln Tyr Thr	100	105	110
Pro Tyr Thr Gly Lys His Leu Asn Asp Met Ile Arg Ile Phe Tyr Met	115	120	125
Lys Ile Ser Glu Leu Ile Glu Arg Lys Val Ser Pro Asn Val Ser Arg	130	135	140
Glu Met Asn Asp Gly Gln Pro Gln Phe Val Pro Asn Leu Phe Lys Lys	145	150	155
Val Tyr Glu Met Ile Ile Ser Lys Pro Asp Val Ser Ala Ala Glu Arg	165	170	175
Ile Gly Lys Ala Leu Phe Lys Leu Gln Ser Lys Ser Arg Glu Leu Glu	180	185	190
Arg Glu Ser Ala Phe Leu Leu Cys Gln His Leu Met Thr Asn Asp His	195	200	205
Gln His Asp Asp Ile Ile Leu Lys Phe Leu Val Ser Gly Val Ser Pro	210	215	220
Trp Tyr Leu His Ser Gln Ile Tyr Met Ser Ser Tyr Lys Leu Gly Phe	225	230	235
Ser Asn Leu Phe Leu Glu Ile Tyr Ala Gln His Tyr Glu Leu Tyr Lys	245	250	255
Ala Asp Pro Ile Tyr Lys Leu Pro Asp Ser Met Thr Leu Leu Asn Glu	260	265	270
Ile Arg Ser Asn Arg Asp Tyr Pro Lys Val Val Asn Ala Ala Lys Asn	275	280	285
Thr Val Gln Val Asn Asn Val Ser Ser Lys Asn Asn Lys Lys Lys Asp	290	295	300
Glu			

305

<210> 141
<211> 155
<212> PRT
<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 141

Ser Glu Ile Asn Ala Thr Ser Thr Tyr His Glu Ile Gly Asp Thr Asn
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Lys Asn Lys Glu Gln Leu Ile Leu Asn Leu Lys Asn His Thr Lys Leu
20 25 30

Ser Glu Gln Lys Lys Lys Thr Asn Leu Leu Val Tyr Asp Ser Gly Ala
35 40 45

Thr Val Ser Val Val Asn Asp Lys Thr Leu Leu Asn Asp Ile Lys Glu
50 55 60

Ser Asn Ile Glu Ile Ala Thr Ala Glu Gly Glu Thr Ser Thr Ala Tyr
65 70 75 80

Ala Leu Gly Thr Leu Thr Ile Ser Val Asn Gly Leu Asn Ala Lys Leu
85 90 95

Asp Gly Val Leu Tyr Leu Pro Ser Ile Gln Leu Asn Leu Ile Ser Ile
100 105 110

Lys Gln Phe Glu Asp Leu Cys Tyr Ala Ile Leu Ile Ser Glu Asn Leu
115 120 125

Met Cys Leu Val His Ser Asp His Gly Pro Thr Val Ile Ala Lys Tyr
130 135 140

Ser Pro Lys Asp Asp Leu Tyr Ser Gly Pro Arg
145 150 155

<210> 142
<211> 795
<212> PRT
<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 142

Met Thr Asn Lys Val Glu Arg Val Thr Tyr Val Ser Ile Arg Asn Ile
1 5 10 15

Lys Gln Glu Val Ala Asp Lys Tyr Met Ile Lys Asp Leu Tyr Tyr Tyr
20 25 30

His Leu Leu Ile Asn His Leu Ser His Glu Lys Leu Gln Leu Leu Val
 35 40 45
 Lys Arg Gly Val Ile Lys Pro Val Lys Ser Thr Ser Ala Glu Ser Ala
 50 55 60
 Ile Leu Asn Cys Gln Ile Cys Val Ala Ala His Ala Lys Leu Ala Ser
 65 70 75 80
 His Asn His Thr Gln Gln Arg Glu Leu Glu Arg Pro Leu Gln Arg Leu
 85 90 95
 His Leu Asp Thr Ala Gly Pro Phe Thr Ser Asn Lys Thr Lys Ser Tyr
 100 105 110
 Leu Thr Thr Val Ile Asp Gln Phe Ser Arg Tyr Thr Glu Val Ile Val
 115 120 125
 Ser Asp Thr Lys Ala Val Lys Gln Ser Ile Leu His Arg Leu Arg Val
 130 135 140
 Trp Asn Asn Arg Phe Gln Phe Lys Ile Ala Glu Ile Arg Tyr Asp Asn
 145 150 155 160
 Ala Leu Glu Tyr Pro Ser Ala Glu Glu Leu Glu Glu Leu Gly Ile Tyr
 165 170 175
 Lys His Leu Leu Pro Asn Tyr Ser Pro Met Leu Asn Gly Thr Ala Glu
 180 185 190
 Ala Thr Asn Arg Pro Ile Val Gln Gly Ile Tyr Lys Val Val Leu Asn
 195 200 205
 Phe Ser Cys Gln Val Leu Ile Leu Phe Pro Phe Ile Val Glu Tyr Ala
 210 215 220
 Val His Ile Arg Asn His Thr Pro Ile Lys Glu Phe Asp Gly Ala Thr
 225 230 235 240
 Pro Tyr Glu Arg Tyr Tyr Gly Leu Ser Lys Tyr Val Ile Pro Phe Phe
 245 250 255
 Gln Phe Gly Thr Asp Val Leu Ile Lys Cys Ala Ser Val Gln Glu Ala
 260 265 270
 Ile Ser Leu Lys Leu Pro Ser Ser Arg Asp Lys Ala Phe Pro Thr Val
 275 280 285
 Met Phe Gly Ala Phe Leu Gly Tyr Gly Ser Asp Ser Phe Thr Phe Arg
 290 295 300
 Val Leu Val Ser Thr Lys Gly Tyr Pro Val Ile Thr Thr Ser Asn Ile
 305 310 315 320
 Arg Pro Ile Ala Thr Met Gln Val Leu Asn Asp Tyr Leu Ala Tyr Ile
 325 330 335

Ser Glu Asn Ser Ser Ile Ser Tyr Asp Asp Thr Phe Leu Ser Pro Leu
 340 345 350
 Asn His Pro Met Ile Arg Thr Asn Gln His Asp Arg Arg Gly Asp Asn
 355 360 365
 Ile Asn Val Glu Tyr Glu Asn Arg Pro Asn Val Pro Phe Glu Tyr His
 370 375 380
 Ala Glu Pro Pro Arg Thr Asn Ser Ser Thr Gly Ile Ile Asp Arg Pro
 385 390 395 400
 Asp Ile Arg Pro Arg Ala Asp Pro Thr Trp Gln Arg Met Pro Asp Ala
 405 410 415
 Asn Ile His Gln Glu Thr Thr Thr Val Gln Thr Pro Asp His Gly Glu
 420 425 430
 Leu Asp Thr Met Ile Asn Asn Glu His Gln Leu Pro Arg Ser Gly Glu
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 450 455 460
 Arg Asp Arg Gly Pro Thr Thr Leu Asn Thr Pro Ile Asp Leu Gly Val
 465 470 475 480
 Pro Asp Glu Thr Asp Asp Ile Ser Met Thr Ser Glu Asn Pro Ile Asp
 485 490 495
 Ser Pro Asn Ser Glu Met Ile Ile Ser Pro Ser Leu Pro Thr Asn Glu
 500 505 510
 Leu Glu His Gln Ile Asp Ile Ser Ser Gly Glu Met Ser Leu Leu Gln
 515 520 525
 Thr Asn Met Glu Ala Asp Asn Glu Leu Lys Thr Asn Glu Met Val Leu
 530 535 540
 Tyr Lys Ser Lys Asn Asp Gly Ile Ile Ile Gln Gln Gln Gln Phe Thr
 545 550 555 560
 Glu Asn Leu Ser Asp Glu Asn Glu Glu Asp Ser Ser Thr Asp Glu Glu
 565 570 575
 Thr Leu Glu Asp Lys Lys Gln Gln Arg Leu Glu Tyr Asn Ile Ser Pro
 580 585 590
 Asn Asp Glu Trp Ile Asn Asn Asp Val Gln Asn Glu Asp Asp Thr Gln
 595 600 605
 Val Pro His Val Lys Glu Pro Ile Asn Tyr Glu Thr Gln Ser Arg Asn
 610 615 620
 Glu Thr Asn Met Pro Arg Ile Glu Met Gly Ile Ile Glu Asn Leu Ser
 625 630 635 640

Asp Asp Gly Lys Asn Thr Pro Arg Glu Leu Arg Ile Val Thr Tyr Asp
645 650 655

Asn Asn Lys Glu Ile Glu Lys Tyr Gln Asp Ser Asn Ile Glu Ile Ser
660 665 670

Glu Pro Arg Asn Glu Asn Glu Asn Gln Thr Phe Ile Glu Ser Asn Leu
675 680 685

Glu Leu Leu Asp Asn Gln Glu Met Phe Gln Glu Asp Pro Gln Val Glu
690 695 700

Asp Ile Arg Leu Thr Thr Pro Lys Lys Asp Lys Ser Leu Ser Pro Asp
705 710 715 720

Phe Asn Gln Thr His Asn Glu Ile Gln Leu Phe Met Ala Asp Ile Asn
725 730 735

Glu Asp Met Leu Glu Glu Tyr Asp Glu Asn Ile Asn Met Asn Glu Val
740 745 750

Leu Ala Asp Ser Thr Glu Thr Leu Asp Lys Glu Leu Asp Leu Asp Glu
755 760 765

Glu Ser Gly Arg Ile Glu Tyr Ile Ala Asp Arg Val Arg Lys Lys Thr
770 775 780

Glu Val Ser Met Val Arg His Thr Gly Asn Ile
785 790 795

<210> 143

<211> 257

<212> PRT

<213> Unknown

<220>

<223> sequence of retrotransposon from unknown organism

<400> 143

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Phe Arg Leu Lys Asp Gly Arg Ala Ser Phe Phe Pro Pro Tyr Lys Thr
20 25 30

Lys Phe Gly Arg Ser Val His Pro Pro Lys Arg Tyr Leu Asn Ala Ile
35 40 45

Val Lys Lys Ile Asp Tyr Asn Gln Lys Glu Trp Arg Gln Ser Met Glu
50 55 60

Glu Glu Ile Glu Lys Phe Lys Ala Asn Gln Val Tyr Thr Val Glu Lys
65 70 75 80

Thr Pro Lys Asn Val Val Pro Leu Lys Thr Met Trp Val His Thr Tyr

85

90

95

Lys Thr Asn Asp Leu Lys Asn His Asn Tyr Lys Ser Arg Cys Val Val
 100 105 110
 Met Gly Asn Tyr Met Val Glu Asn Arg Asp Phe Asp Pro His Ala Ile
 115 120 125
 Ser Ser Pro Val Val Asp Leu Thr Ser Ile Arg Leu Leu Ser Ala Ile
 130 135 140
 Ala Val Glu Asn Asn Leu Val Met His Gln Leu Asp Ile Ala Ser Ala
 145 150 155 160
 Tyr Leu Asn Ala Ser Leu Glu Asp Gly Arg Val Ile Phe Val Arg Pro
 165 170 175
 Pro Arg Gly Phe Glu Val Lys Pro Gly Tyr Ser Trp Arg Leu His Lys
 180 185 190
 Ser Val Tyr Gly Leu Arg Gln Ser Ala His Asn Trp Tyr Ser His Phe
 195 200 205
 Lys Asn Val Leu Glu Ala Asn Gly Leu Lys Gln Thr Leu His Asn Asp
 210 215 220
 Gly Ile Phe Trp Lys Asn Tyr Glu Asn Gly Asp Val Leu Tyr Val Ser
 225 230 235 240
 Val Tyr Val Asp Asp Val Phe Ile Lys Ala Asn Ser Met Ser Leu Cys
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Asn

<210> 144

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<212> DNA

<213> Unknown

<220>

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<400> 144

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 ccaaataatta aacatccact cggattcaaa tacctcagca ctcttttata ggcacttgta 240
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 tgggaaacag atttgaccat ctaactttca tggttcttat gaaaaagatc tggaaatggt 360
 gatatagctt gattgtctag catattcagc gattacccta ttttgtggtt gcctgggata 420

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caactagctg gctattttccc tggatagaaa accttcattc ttctttctct ggttgagtat	600
caccgacttg tggcctgacc gttcaacccc ctacaataca ccatcaactt tatacttgta	660
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ataaataagg gtatgaaata ccaacatccc agaatatcaa cgagatagaa gggaggagtt	180
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acacgctcaa tctcaggtaa agaaagtta tattccatca	280

<210> 146
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<212> DNA
<213> Candida albicans

<400> 146
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11

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<210> 150

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<400> 150
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32

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<400> 151
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<400> 152
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32

<210> 153
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<400> 153
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25

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<400> 154
gcgtctagaa attctgtacc ttc

23

<210> 155
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<400> 155
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24

<210> 156
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<400> 156
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18